

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 15:20:30 ; Search time 2213 Seconds

(without alignments)
10297.785 Million cell updates/sec

Title: US-09-870-501-2

Perfect score: 1089

Sequence: 1 cttctagggtcgtccgcgat.....gaataaaaaaaaaaaaaa 1089

Scoring table: IDENTITY_NUC

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_higo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	1089	100.0	1089	8	AB063117	AB063117 Hordeum v
2	511	46.9	1167	8	AF159254	AF159254 Zantedesc
3	475.8	43.7	1239	8	GHU37060	U37060 Gossypium h
4	449.4	41.3	1238	8	AF139190	AF139190 Mesembrya
5	444.4	40.8	1133	8	AB070626	AB070626 Cucurbita
6	438.6	40.3	1177	8	AT069138	U69138 Arabidopsis
7	437	40.1	1045	8	ATAPEXT	X88276 A.thaliana
8	437	40.1	1121	8	AY065143	X8065143 Arabidops
9	437	39.8	1138	8	ATAPX	X8003 A.thaliana
10	433.6	39.8	1127	8	AF442387	AF442387 Capsicum
11	303.6	27.9	1229	6	AR074176	AR074176 Sequence
12	303.6	27.9	1229	6	BD005724	BD005724 Materials
13	301.4	27.7	1138	8	AF411228	AF411228 Hordeum v
14	293.8	27.0	1042	8	ZMAPXG	Z24934 Z.mays apx
15	290.8	26.7	1012	8	AF159627	AF159627 Fragaria
16	290.8	26.7	1058	8	AB050724	AB050724 Oryza sat
17	290.8	26.7	1160	8	AB053297	AB053297 Oryza sat
18	290.2	26.6	1040	8	AF159628	AF159628 Fragaria
19	286	26.3	1040	8	NTU15933	U15933 Nicotiana t
20	285.4	26.2	1035	8	AF159633	AF159633 Fragaria
21	285.4	26.2	1040	8	AF039953	AF039953 Fragaria
22	285.4	26.2	1065	8	AF159632	AF159632 Fragaria
23	284.8	26.2	1108	8	AF378131	AF378131 Zantedesc
24	282.8	26.0	1044	8	AF022213	AF022213 Fragaria
25	282.8	26.0	1097	8	AF053474	AF053474 Zantedesc
26	282.4	25.9	1050	8	HVU6	AJ006358 Hordeum v
27	282.2	25.9	1035	8	AF159630	AF159630 Fragaria
28	282.2	25.9	1051	8	AF159631	AF159631 Fragaria
29	281.2	25.8	1030	8	AF159629	AF159629 Fragaria
30	280	25.7	983	8	D45423	D45423 Rice mRNA f
31	278.8	25.6	756	8	ATAPCYT	X88275 A.thaliana
32	278	25.5	1055	8	TOBTCAP	D65912 Nicotiana t
33	277	25.4	753	8	AB078600	AB078600 Brassica
34	274.2	25.2	1117	8	VU061379	U61379 Vigna ungu
35	272.2	25.0	753	8	AB078599	AB078599 Brassica
36	271.4	24.9	1095	8	MCU43561	U43561 Mesembryant
37	270.6	24.8	753	8	RSAPX	X78452 R.salivus (
38	269.4	24.7	1023	8	ATASCOR	X59600 A.thaliana
39	269.4	24.7	1059	8	AY039879	AY039879 Arabidops
40	269.4	24.7	1060	8	AY056395	AY056395 Arabidops
41	269.2	24.7	1069	8	D88649	D88649 Cucumis sat
42	267.8	24.6	1064	8	GM056634	U56634 Glycine max
43	267.4	24.6	1069	8	SP1ASCPR	L20864 Spinacia ol
44	267.4	24.6	1083	8	SPICAP	D58664 Spinacia ol
45	267.2	24.5	1054	8	PSAPXI	X62077 P.sativum A

ALIGNMENTS

RESULT 1
AB063117
LOCUS
DEFINITION Hordeum vulgare HvAPX1 mRNA for peroxisome type ascorbate
ACCESSION AB063117
VERSION
KEYWORDS
SOURCE
ORGANISM
Hordium vulgare (cultivar:Haruna-nijo) early growth stage cDNA to
mRNA, clone:lib:barley leaf cDNA.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 1089)
REFERENCE
AUTHORS Shi,W.M., Muramoto,Y., Ueda,A. and Takabe,T.
TITLE Cloning of peroxisomal ascorbate peroxidase gene from barley and
enhanced thermostolerance by overexpressing in Arabidopsis thaliana
JOURNAL Gene. 273 (1), 23-27 (2001)
MEDLINE 21376122
REFERENCE 2 (bases 1 to 1089)
AUTHORS Takabe,T.
TITLE Direct Submission

/db_xref="GI:5442410"
/translation="MAAPVADGYLKEVDKARBDLALIAKNCAPVMLRLAMDAGT
YDVAKTGGPNKSIINEEHRKAGNAKIKIDICEYKAKHPRTTYADLYAGVVA
VEWNGPPTIDEPGRDLSVPKREGRDLDAOGSAHLDDVYRMLISPKDIYALSGH
TLGRAHPERSGDPMTNEPKFNDYSVELLECKRELLKIPDKXIVEDPERGCV
ELKXEDAEFRFDYAKESHKLSLELFTSPKASKSADHTSTLLAOSAVAVAAVVF
LSTCEVRSRRK"
BASE COUNT 326 a 249 c 280 g 312 t
ORIGIN

Query Match 46.9%; Score 511; DB 8; Length 1167;
Best Local Similarity 75.0%; Pred. No. 7e-117;
Matches 656; Conservative 0; Mismatches 210; Indels 9; Gaps 1;

19 ATGGCGGCTCCCGTGGTGGACCCGAGTACCTGCGCCAGTGGACAGGCGCGCCGCC 78
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
52 ATGGCGGACCGGTGGTGGACCGCGCTACCTCAAGAGGTGGACAGCGCGCGAGGAC 111
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
79 TTCCGTGCCCTCATGCGCTCCAAAGGAGTGGCCCATGCTCCGCTCGCATGGCAT 138
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
112 CTCCCGCGCCCTCATGCGCGAGAAAGTCCCTCCGCTCATGCTCCGCTCATGGCAT 171
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
139 GATGCGGACCTATGATGTGAACAAAGACTGGTGGTCAAAATGCTCAATTTAGATAC 198
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
172 GATGCGGACCTATGATGTGAACAAAGACTGGTGGTCAAAATGCTCAATTTAGATAC 231
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
199 GAGGAGAGTACACCATGTTCAATGCTGGCTTAAATTTGCTATTTGCTCTTGGAG 258
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
232 GAGGAGAGTACACCATGTTCAATGCTGGCTTAAATTTGCTATTTGCTGTA 291
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
259 CCTATTAAAGCAAGCATCAAAATTTAGATGTGACAGCTTTCATGAGTGGCGAGTA 318
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
292 ACGGTGAAGCAAAACATCAAGATTAACATATGCTGACCTTTACAGCTTCTGGAGAT 351
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
319 GTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 378
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
352 GTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
379 TCAGTTTTCCTCCCGTGGTGGACCCGAGTACCTGCGCCAGTGGACAGGCGCGC 438
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
412 TTGGTTTTCCTCCCGTGGTGGACCCGAGTACCTGCGCCAGTGGACAGGCGCGC 471
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
439 GATCTCTTTTATGCAATGGGTTTAAACAGCAAAATTTGATGAGTGGGCGGAC 498
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
472 GATCTCTTTTATGCAATGGGTTTAAACAGCAAAATTTGATGAGTGGGCGGAC 531
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
499 ACCCTGGGAAAGGCGCTGGAAGGCTGGGTTGAGGCGTGAAGTGGTGGACCT 558
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
532 ACATTTGGGAAAGGCGCTGGAAGGCTGGGTTGAGGCGTGAAGTGGTGGACCT 591
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
559 CTGAAATTTGACAACTCATCTTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 618
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
592 CTGAAATTTGACAACTCATCTTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 651
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
619 AAGCTCCTTACTGATAGGCTATTTGATGATCTGAAATTTGAGCGTGTGAGCTT 678
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
652 AAGCTCCTTACTGATAGGCTATTTGATGATCTGAAATTTGAGCGTGTGAGCTT 711
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
679 TATGCAAAAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 738
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
712 TTTGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
739 GAATCTGGCTTACACACAGGAGTGGCCAGCATCTACAAAATTCAGATTTTCAAT 798
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
772 GAATCTGGCTTACACACAGGAGTGGCCAGCATCTACAAAATTCAGATTTTCAAT 822
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
799 GCTGTGTTACTTGCACAGAGTGCAGTGGGGTACAGATTTGTCAGCTGTATTCGGC 858
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
823 ACCACTACTTATAGCTACAGAGCTGTGGAGTGGCTGTGCTGTGTGTCTTA 882
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
859 GGCTACCTGTAGAGCTTCCAAAGAGGAGCAAGTA 893
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
883 ACTTACTGCTATGAAGTATCTAGAGAGCAAGTA 917
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

RESULT 3
GH037060 1239 bp mRNA linear PLN 23-APR-1997
LOCUS GH037060
DEFINITION Gossypium hirsutum ascorbate peroxidase mRNA, complete cds.
ACCESSION U37060
VERSION U37060.1 GI:1019945
KEYWORDS
SOURCE upland cotton.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE
1 (bases 1 to 1239)
Bunkelmann, J. R. and Trelease, R. N.
Ascorbate peroxidase. A prominent membrane protein in oilseed
91yoxsomes
JOURNAL Plant Physiol. 110 (2), 589-598 (1996)
MEDLINE 96351186
REFERENCE 2 (bases 1 to 1239)
Trelease, R. N.
JOURNAL Direct Submission
Submitted (23-SEP-1995) R. N. Trelease, Botany, Arizona State
University, Tempe, AZ 85287-1601, USA
FEATURES
source
1..1239
/organism="Gossypium hirsutum"
/cultivar="Deltapine 62"
/db_xref="taxon:3635"
94..960
/note="glyoxysomal membrane-bound protein"
/product="ascorbate peroxidase"
/protein_id="AAB52954.1"
/db_xref="GI:1019946"
/translation="MAAPVADGYLKEVDKARBDLALIAKNCAPVMLRLAMDAGT
YDVAKTGGPNKSIINEEHRKAGNAKIKIDICEYKAKHPRTTYADLYAGVVA
VEWNGPPTIDEPGRDLSVPKREGRDLDAOGSAHLDDVYRMLISPKDIYALSGH
TLGRAHPERSGDPMTNEPKFNDYSVELLECKRELLKIPDKXIVEDPERGCV
ELKXEDAEFRFDYAKESHKLSLELFTSPKASKSADHTSTLLAOSAVAVAAVVF
LSTCEVRSRRK"
BASE COUNT 346 a 262 c 287 g 344 t
ORIGIN

Query Match 43.7%; Score 475.8; DB 8; Length 1239;
Best Local Similarity 72.1%; Pred. No. 4.4e-108;
Matches 637; Conservative 0; Mismatches 237; Indels 9; Gaps 1;

12 GTCCGGATGGCGGCTCCGGTGGTGGACCGCGATGCTGCGCGAGTGGACAGGCGCG 71
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
87 GACTTCAATGCGGCTTCCAGTATGATGATGATGATGATGATGATGATGATGATGAT 146
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
72 CCGCGCTTCCGCTCCGCTCATGCTCCAAAGGATGCGGCCCATCATGCTCGCTCGC 131
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
147 TCGAGACCTTCCGCGCTCATGCTCCGCTTGAAGATTTGCGCTCATCATGCTCGCTTAC 206
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
132 ATGGCATGATGCTGGACCTATGATGATGATGATGATGATGATGATGATGATGATGAT 191
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
207 GTGGACGATGCTGGGACCTATGATGATGATGATGATGATGATGATGATGATGATGAT 266
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
192 TGAATPACGAGAAAGATACACCATGCTCAATGCTGATGCTTAAATTTGCTATTGATCT 251
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
267 AAGGAATGAAGAGATTACATCATGCGCCCAATAGCGCTTGAATTTGCTATTGATTT 326
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
252 CCTGAGCCTATTAAAGCAAGCATCCAAAGATTACATGAGAGCTTCAATGAGCTTGC 311
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
327 TTGTGAGGAAGTGAAGGCTAAACATCTTAAATTTAGCTATGACAGACCTTATACAGCTTGC 386
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
312 CCGAGTATGCTGAGTGAAGTACCGGGGCTCCAAACCTTGAATTCATCTCTGGAAGACG 371
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
387 TGTGTGTGCTGTGTAAGTCACTGAGAGTCTTCAATTTGATGCTGGAAGAA 446
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

QY	372	TGATTCGTCAGTTGGTCCCGCTGAGAGACGCCCTCCGATGCTGAAGAAAGTGACACACA	431
Db	447	GGATTCMAACATTTCGCCCGAGGMAAGGCCGCACTTCCAGATGCTMAAAGAGGTGCACCTTA	506
QY	432	TCCTAAGGACATCTTTTATCGAATGGGGTTTAAACAGACAAAGATATTTGTAGCACTATCTGG	491
Db	507	TCCTGAGGGGACATCTTCTATCGAATGGGTCCTGCTGCAAAAGATATTTGTGGCATTTATCTGG	566
QY	492	GGGGGACAGCCCTGGGAAAAGGCGCATCTGTAAGAGTCTGGGTTTGAACGTGCATGACCTCG	551
Db	567	GGGTACACACTGGGGAAGGGCTCATCTGAGAGATCAGGTTTTGTAGTGGCCCTTGGACCAA	626
QY	552	TGACCCCTGGAATTTGACACATCATCTATCTTTGTTGAGCTAGAGGGGGAATCTGACGG	611
Db	627	TGAACCCCTGGAAGTTGACACACTCTTACTTCTTGAGCTGCTMAAAGGGGAATCTGMAAG	686
QY	612	TCCTTGAAGCTCCCTACTGATTAAGGCATTTGTTGATGATTCCTGAATTTGACAGCTTAGT	671
Db	687	GCTTTTGAACCTTCCAAACGACAGAGCTTTGTTAGATGACCCCTGAGTTCCCAAGATATG	746
QY	672	GGAGCTTATGCAAAAGATGAGAGATGTTTCTTCAAGGCTACGCGTGAATCATCACAAAA	731
Db	747	CGAGCTCTAGTCCAAAGATGAGATGCGCTTCTTCAGAGTTACGCGGAATCTCATAGAA	806
QY	732	ACTTTCTGAACCTTGCGCTTCACACAGAGAGAGAGCGCCGACGATCTACAAAAATCAGATG	791
Db	807	ACTTTGCGAAGCTTGGGTTTACTCTC-----CACTTAGCTCGGCTCCAAAGTATGAT	857
QY	792	TTCAACTGCTGTGTGTACTTGCACACAGATGCAAGTGGGGTATAGCATTTGCTGCACTGTACT	851
Db	858	GAAGGACAGACACTGTATTGGCACAGGGTCTCTGGGGGGTGTGTGTGCGCGCCGACAGTGT	917
QY	852	TATCGCGGCTACCTGTACAGAGCTTCCAAAGAGGAGCAATGA	894
Db	918	GATCCTAGCTACTTTTACGAGGTCGCGCAAAAGATGAAGTGA	960

RESULT 4

AF139190 1238 bp mRNA linear PLN 16-MAY-1999

LOCUS AF139190

DEFINITION Mesembryanthemum crystallinum cytosolic ascorbate peroxidase mRNA,

complete cds.

ACCESSION AF139190

VERSION AF139190.1

KEYWORDS GI:4835908

SOURCE .

ORGANISM common ice plant.

Mesembryanthemum crystallinum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.

1 (bases 1 to 1238)

Michaelowski,C.B. and Bohnert,H.J.

A putative cytosolic ascorbate peroxidase cDNA (AsX5) from the

common ice plant

unpublished

2 (bases 1 to 1238)

Michaelowski,C.B. and Bohnert,H.J.

Direct Submission

Submitted (30-MAR-1999) Blochmistry, University of Arizona, Bio

Sciences West 513, Tucson, AZ 85721, USA

Location/Qualifiers

1..1238

/organism="Mesembryanthemum crystallinum"

/db_xref="taxon:3544"

/tissue_type="leaves; roots"

111..974

/note="similar to L0-328, R6-3, L72-2"

/codon_start=1

/product="cytosolic ascorbate peroxidase"

/protein_id="AAD30294.1"

/db_xref="GI:4835909"

/translation="MAMPVPVDSYLKEIDKARDRLALISNRSCADIMRLAWHDAG

BASE COUNT	328 a	275 c	297 g	338 t	ORIGIN
Query Match	41.3%;	Score 449, 4;	DB 8;	Length 1238;	
Best Local Similarity	70.1%;	Pred. No. 1,76-101;			
Matches 623;	Conservative 0;	Mismatches 221;	Indels 15;	Gaps 1;	
QY	10 TCGTCCGCGATGGCGGCTCCGGTGGTGGACGGCCGATACCTGCGCCAGGTGCACAGGCGG	69			TYCARTKGTGANGSIIRNEEEXVHANNLKKALIDCDEEYKAYPIITFADILYOLAGVY
Db	105 TCATCAATGGCGATGGCCACCGGGTGGCGACAGTGTGTACTCTCAAGAAATCGACAAGCT	164			AVEVGGPTIEFVPERKDSKSTINEGRLPAKGGPHLDIFVPMGLDKDILVALSGV
QY	70 CGCGCGCCCTTCGGTGGCCCTTCATCGCTCCCAAGGGATGGCCCCCATCATGCTCCGCC	129			HLKHAHPEPSFQDPWTEPLKFDNSYFWEILKGSSEGLDLPDKLVDPAPFRP
Db	165 CGTGGCATTTTGACACACTCATCTCTAAVTCGACAGCTCGCTCTCATATGCTCCGCTC	224			VELXAKDEAPSRDPAVSHKLSLELGTTPSGSSSGKRDSTIIAAGVAVAAAVYIIL
QY	130 GCATGGCATGATCTGGCACCTATGATGTGAACACAAAGACGTGGTGGCAAAATGGTTCA	189			STIEFERLRK*
Db	225 GCGTGACGACAGCCTGGAGCGATTTGTGGAGAAAGAAACCGGTGGCGGTATMGCTCC	284			
QY	190 ATTGATACAGAGAAAGTACACCCATGGTTCAAAATCTGGCTTTAAAAATTCCTATTGAT	249			
Db	285 ATTGAGACAGGAAAGATGACCTACAGCGCCCAACATGGATTGAAGAAAGCATTTGAT	344			
QY	250 CTCCTTGAGCCTATTAAACGGAAGATCCAAAGATTACATTCAGACCTTCATCAGCTT	309			
Db	345 TGTGTGTGAGAGGTGAAGGCTAAATATCCAAAGATCAATATGCTGACATATATCAGCTT	404			
QY	310 GCGGAGTAGTTCAGATTAAAGTACACCGGGGGTCCACCGTTGATTCATCCTGGAGA	369			
Db	405 GCTGTGTGTTGTCAGATTGAATCACTGGAGGGCCGACATTGAATTTGTCCTGGTAGA	464			
QY	370 CGTGATTCGTCATTTGTCCCGGTGAAGAGACGCTTCGTGATGTAGAAAGGTGACCA	429			
Db	465 AAGACTCAAAAGTATCTCAAAACAGAGGGAGACTCCAGATGGGAAAAAAGGTCCACCA	524			
QY	430 CATCTAAGGAGACATCTTTATCGAATGGGGTTAAACAGACAAAGATTTAGACATATCT	489			
Db	525 CATGTGAGGATTAATTTATCGATGGGTGTCACTGACAAAGACATTTAGGCCCTTTCA	584			
QY	490 GGGGGCACAGCTGGGAAAGGCGCATCTTGAAGGTCTGGGTTTGACGGTGCATGACT	549			
Db	585 GGGGCTCATACCTGGGAAGGGACATCAAGAGGCTCCGGTTTGTATGGCCCATGGACC	644			
QY	550 CGTGACCTCTGAAATTTGACAACATCACTTCTTGAGCTACTGAAGAGGGGAAATGTGAG	609			
Db	645 CAGAGGCTGTCAAGTTTATATCTCTATTTTGTGGAGCTGCTGGAAGGGAATATAGG	704			
QY	610 GGTCTTGAAGCTCCCTACTATTAAGCATTTGGATGTGATCTGTGAATTTGAGCGTAT	669			
Db	705 GGAATTTGGAGCTTCTCAAGATTAACATTTGGTGGAGGATCCTGCATTTGCCCTTAT	764			
QY	670 GTGAGATTATCAAAAGATGAGGATGTTTCTTCAAGGACTAGCGTGAATATACACAA	729			
Db	765 GTTGAACGTATCTTAAGATTAAGATGCTTTCTTCGTGACTACGCTGATATACCAAG	824			
QY	730 AAACCTTGTGAACCTTGACACACAGGAGACAGTGGCCGACATCTCAAAATATGAT	789			
Db	825 AAACCTTGTGAACATAGATTATCTCCAAAGCGG-----GTCCAAAGTAGGT	869			
QY	790 GTTTCACATGCTGTACTTGCACAGAGTGCAGTGGGGTAGCAGTTGCTGCAGCTGTA	849			
Db	870 CCTAAGGACAGCATTAATTGGCTCAAGGTGCTGTGGGGTTGGAGTGGCTGCAGCTGCG	929			
QY	850 GTTATGCGGGGCTACTCTAGACACTTCAAGAGGAGCAAGTAAGGGGTT	900			
Db	930 GTATCTCTGAGCTACTCTTTGAAGTACGCAAAAGACTCAAGTGAAGAGAT	980			

RESULT 5
AB070626 1133 bp mRNA linear PLN 05-SEP-2001
DEFINITION Cucurbita sp. cv. Kurokawa Amakuri PAPX mRNA for peroxisomal ascorbate peroxidase, complete cds.
ACCESSION AB070626
VERSION AB070626.1 GI:15430583
KEYWORDS
SOURCE
ORGANISM Cucurbita sp. cv. Kurokawa Amakuri (cultivar:Kurokawa Amakuri) CDNA to mRNA.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
REFERENCE 1 (bases 1 to 1133)
AUTHORS Nito,K., Yamaguchi,K., Kondo,M., Hayashi,M. and Nishimura,M.
TITLE Pumpkin peroxisomal ascorbate peroxidase is localized on peroxisomal membranes and unknown membranous structures
JOURNAL Plant & cell physiology. 42 (1), 20-27 (2001)
MEDLINE 21109356
REFERENCE 2 (bases 1 to 1133)
AUTHORS Nito,K. and Nishimura,M.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2001) Kazumasa Nito, National Institute for Basic Biology, Dept. Cell Biol., Myodaiji, Okazaki 444-8585, Japan (E-mail:nitokazen@nib.ac.jp, Tel:81-564-55-7504, Fax:81-564-55-7505)
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Best Local Similarity 70.3%; Pred. No. 3e-100;
Matches 617; Conservative 0; Mismatches 246; Indels 15; Gaps 1;
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QY 317 TAGTTGCAATGAGTCAACCGGGGGTCCACCGCTTGAAGTATCCCTGGAAGACGTAT 376
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DEFINITION
ACCESSION U69138
VERSION U69138.1 GI:2444018
KEYWORDS
SOURCE
ORGANISM
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidops.
REFERENCE 1 (bases 1 to 1177)
AUTHORS Zhang,H., Wang,J., Nickel,U., Allen,R.D. and Goodman,H.M.
TITLE Cloning and expression of an Arabidopsis gene encoding a putative peroxisomal ascorbate peroxidase
JOURNAL Plant Mol. Biol. 34 (6), 967-971 (1997)
MEDLINE 97435981
REFERENCE 2 (bases 1 to 1177)
AUTHORS Zhang,H., Wang,J., Nickel,U., Allen,R.D. and Goodman,H.M.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1996) Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409, USA
COMMENT On Sep 30, 1997 this sequence version replaced g1:2435396.
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LOCUS			
DEFINITION	A.thaliana mRNA for ascorbate peroxidase, extraplastidal (membrane bound) (APX3).	1045 bp	linear
ACCESSION	X98276		
VERSION	X98276.1	GI:1523790	
KEYWORDS	ascorbate peroxidase.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
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AUTHORS	1 (bases 1 to 1045) Karpinski, S., Escobar, C., Karpinska, B., Creissen, G. and Mullineux, P. M.		
TITLE	Photosynthetic electron transport regulates the expression of cytosolic ascorbate peroxidase genes in Arabidopsis during excess light stress		
JOURNAL	Plant Cell	9 (4), 627-640	(1997)
MEDLINE	97290209		
REFERENCE	2 (bases 1 to 1045)		
AUTHORS	Escobar, C.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-JUN-1996)	C. Escobar, John Innes Centre, Applied Genetics, Colney, Norwich, NR4 7UH, UK	
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QY	136	CATGATGCTGGACACCTATATGTGAACACAAAGAACTGGTGGTGAATAATGTTAATTAGA	195
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QY	196	TACGAGAAAGGATACACCATTCGTCATATGCTGATATGATATGCTTCT	255
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DEFINITION	Arabidopsis thaliana L-ascorbate peroxidase (At4g35000; M4E13.60)		
ACCESSION	AY065143		
VERSION	AY065143.1		
KEYWORDS	PII, CDNA.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons: core eudicots: Rosidae: eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1121)		
AUTHORS	Nguyen, M., Karlin-Neumann, G., Southick, A., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carinluci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, Y., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, X., Narusaka, M., Pham, P. K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shin, P., Yamada, K., Shinozaki, K., Ecker, J., Rheologis, A. and Davis, R.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-DEC-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,		

Db 446 TCAAATGCTGCCCCAAGAGAGACCTTCGATGCCAACAAGCTTCCAAACATCTC 505
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RESULT 9

ATAPX 1127 bp mRNA linear PLN 04-SEP-1997
LOCUS A.thaliana mRNA for ascorbate peroxidase.
DEFINITION X98003
ACCESSION X98003.1 GI:1332438
VERSION APX gene; ascorbate peroxidase.
KEYWORDS thale cress.
SOURCE ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (bases 1 to 1127)
AUTHORS Jespersen, H.M.
TITLE Direct Submision
JOURNAL Submitted (21-MAY-1996) H.M. Jespersen, University of Copenhagen,
Department of Protein Chemistry, Oester Farimagsgade 2A, DK-1353
Copenhagen K, DK-1353 Copenhagen K, Denmark

REFERENCE 2 (bases 1 to 1127)
AUTHORS Jespersen, H.M., Kjaergaard, I.V., Ostergaard, L. and Welinder, K.G.
TITLE Arabidopsis thaliana: three novel ascorbate peroxidases from
types of ascorbate peroxidase

JOURNAL Biochem. J. 326 (Pt 2), 305-310 (1997)
MEDLINE 97419079

FEATURES

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BASE COUNT 323 a 245 c 273 g 286 t
ORIGIN

Query Match 40.1%; Score 437; DB 8; Length 1127;
Best Local Similarity 69.6%; Pred. No. 2,1e-98;

Matches 612; Conservative 0; Mismatches 255; Indels 12; Gaps 1;

OY 16 GCCATGGCGGCTCCGGTGGTGGACGCCGAGTACTCGCCAGGTGACAGGCGCGCCG 75
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QY 856 GCGGCTACCTGTACGAGCTTCGCAAGAGGACCACTAA 894
 DB 896 TTGGTACTTACGAGATCCGAGAGAGATGAAGTAA 934

RESULT 10
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 DEFINITION AF442387
 ACCESSION AF442387
 VERSION AF442387.1 GI:17066704
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 ORGANISM Capsicum annum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
 REFERENCE 1 (bases 1 to 1138)
 Hwang, B.K. and Do, H.M.
 Pepper ascorbate peroxidase and thiolredoxin peroxidase genes
 regulate H2O2 accumulation and peroxidase activity during the
 bacteria-induced hypersensitive reaction in Capsicum annum
 Unpublished
 2 (bases 1 to 1138)
 Hwang, B.K. and Do, H.M.
 Direct Submission
 Submitted (02-NOV-2001) College of Life and Environmental Science,
 Molecular Plant Pathology Laboratory, Korea University, Anam-dong,
 Sungbuk-gu, Seoul 136-701, Republic of Korea
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RESULT 11
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 LOCUS
 DEFINITION Sequence 85 from patent US 5952486.
 ACCESSION AR074176
 VERSION AR074176.1 GI:10000936
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1229)
 Bloksberg, L.N., Havukala, I. and Grierson, A.W.
 Materials and methods for the modification of plant lignin content
 Patent: US 5952486-A 85 14-SEP-1999;
 JOURNAL Location/Qualifiers
 FEATURES
 source
 1. 1229
 /organism="unknown"
 BASE COUNT 342 a 256 c 292 g 339 t
 ORIGIN

Query Match 27.9%; Score 303.6; DB 6; Length 1229;
 Best Local Similarity 63.4%; Pred. No. 4.5e-65;
 Matches 465; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

QY 16 GCGATGCGGCTCCGGTGTGACGCGGAGTACCTGCGGAGTGCACAGGCGCGCCG 75
 DB 222 GTGAAGGCTTATCCACCGTAAGCGAGAGTACAAAGCTGCCATTGCAAAATGCAAGAG 281
 QY 76 GCTTCGCTGCTCATGCTCCACAGGATGCGCCCATCATGATGCTCGCTCGATG 135
 DB 282 AAGCTTCGAGCTCTCATGCTCAGAGAACTGTGCGCCCATCATGATGCTGAATCCGATG 341

QY	136	CATGATGCTGGCACCATTATGTGAACACAAGAAAGTGTGTGCATAAGTGCTCATTAAGA	195
Db	342	CACAGCGCTGGACTTACGATGTCAAGACCAAGACCGGAGGCCCTTCGGAGAGATGA	401
QY	196	TACGAGGAGAGATCACCCATGTTCAAATGCTGGCTTAAAAATTGCTATTGATCTCTT	255
Db	402	TATGGGCGCAGGTTGCTCCCAAGGTGTAAACAGTGGCTGGACATCCGATTAAGCTCCG	461
QY	256	GACCTATTAAACGAAAGCATCCAAGATTACATATGACAGACCTTGATAGCTTGGCCGA	315
Db	462	GAGCCATACAGAGAACAGTTCCCATATATACCTATATGTAAGCTTATATAGTTGGCTGT	521
QY	316	GTATGTTCAGTTGAGTACACCGGGGGTCCAAACGGTTGAGTTCACTCCCTGGAAAGCTGAT	375
Db	522	GTGGTGGCTGTGTTAAGTAGACCGGGGACCTGACATTCCTGATCCCTGGAAGAAAGAC	581
QY	376	TGTCAGTTTGTCCCGTAGAAGGACGCTTCTCGATGCTAAGAAAAGTGCACACATCTA	435
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Db	642	AGGAGTGTTTTGTGTACANTGGGGTTGAATGATNAAGAAATGTGGCCCTGTCTGGTGGC	701
QY	496	CACAGCCTGGGAAAGGCGCATCTGAAAGGTCTGGTTTTGAGGTGCATGAGACTGTGAC	555
Db	702	CACACTTTGGGGGATGCCACAAGGAGATCTGTTTGAAGGACCATGAGACTCTTAAC	761
QY	556	CCCTCAAAATTTTACAAACATCTTCTTGAGCTACTGAAGGGGAAATCTGAGGGTCT	615
Db	762	CCCCATATCTTGACAACTCTTACTTCACAGAGCTGTGATCTGAGAGAAAGAGGCTGG	821
QY	616	CTGAGCTCCCTACTGATTAAGGCATTTGGATGATCGTAAATTCGACGCTATGTGAG	675
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Db	882	AAGTATGACACAGGACCAACGCTTCTTTCCTGCTGATTAACGGAACCTCAAGCTT	941
QY	736	TCTGACTTGGCTT 749	
Db	942	TCTGAACCTTGGGTT 955	
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BD005724			
LOCUS	BD005724	1229 bp	DNA linear PAT 31-JAN-2002
DEFINITION	Materials and methods for the modification of plant lignin content.		
ACCESSION	BD005724		
VERSION	BD005724.1	GI:18634095	
KEYWORDS	JP 2001500378-A/85.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 1229)		
AUTHORS	Blosberg,L.N., Grierson,A.W. and Hawukkala,I.J.		
TITLE	Materials and methods for the modification of plant lignin content		
JOURNAL	Patent: JP 2001500378-A 85 16-JAN-2001;		
	GENESIS RESEARCH & DEVELOPMENT CO LTD, LETCHER CHALLENGE FORESTS		
LTD			
OS	Unidentified		
PN	JP 2001500378-A/85		
PD	16-JAN-2001		
Pf	10-SEP-1997 JP 1998513535		
PR	11-SEP-1996 US 08/7113000		
PI	LEONARD NATHAN BLOKBERG,ALISTAIR WALLACE GRIERSON, PI		
JAARKO HAVUKALA			
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Strandedness:	Single;		
CC	Topology: Linear;		
FH	Key Location/Qualifiers		

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Query Match	27.9%	Score 303.6	DB 6	Length 1229	
Best local Similarity	63.4%	Pred. No. 4.5e-65			
Matches 465	Conservative 0	Mismatches 269	Indels 0	Gaps 0	
QY	16	GGCATGGCGGCTCCGGTGGTGAGCGCCGAGTACCTCGCCAGGTGCACAGGCGCGCGC	75		
DB	222	GTCGAAGGCTTATCCACCCGTAAACGAGAGTACAAAGGCTCCATTGACAAATGCAAGAG	281		
QY	76	GCGTTCGGGCGCCCTCAGCCGCTCCAGGAGATGGCGCCCATCATGTCTCGCTCGATG	135		
DB	282	AACTCCGAGCTCTCATCTGTCAGAGAAAGACTGGCCCGCATATGGTTGAAATTCGATG	341		
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DB	342	CACAGGCGCTGGGACTTACGATGTCAAGACCAAGACCGGAGGCGCTTCGGAGCATGAGA	401		
QY	196	TACGAGAAAGATACACCCATGGTTCAAAATGCTGCTTAAAAATTTGCTATTGATCTCT	255		
DB	402	TATGGGGCGGAGCTGCCACGCTGTAAAGAGTGTCTGAGACATGCAGTTTAGGCTCTG	461		
QY	256	GAGCCTATTAAAGCGAAGCATCCAAAGATTACATATGACAGACCTTATACGCTTGCCGA	315		
DB	462	GAGCCTATCAAGAACAGTATCCCATTAATCACCTATGCTGACCTTTATGATGGCTGT	521		
QY	316	GTAGTTGCAAGTGAATCTACCGGGGGTCCACCGTTGAGTTATCCCTGGAAGAGCTGAT	375		
DB	522	GTGGTGGCTGTGTAAGTGAACGCGGAGACCTGACATTCCGTTCCATCTCTGAAAGAGAC	581		
QY	376	TGCTCAGTTTGTCCCGGTGAAGAGACGCTCTGATGCTAAGAAAGTGCACACATCTA	435		
DB	582	AAGCCTGAGCCTCCAGAAAGAGGCGCCTTCGTGATGTAACAAAGAGACCTGATCATCG	641		
QY	436	AAGGACATCTTTATATGAAATGGGGTTTACACAGACAAGATATTGTAGACTATCTGGGGG	495		
DB	642	AAGGAATGTTTTGGTACATAGGGGTGTAATGATTAAGAAATTTGGGCCCTTGTCTGTG	701		
QY	496	CACAGCCTGGGAAAGCGGATCCTGAAGAGTCTGGGTTGACGGTGCATGACCTGTGAC	555		
DB	702	CACACCTTGGGGAGATGCCAAGAGAGATCTGGTTTGAAGAGACCATGACCTCTAAC	761		
QY	556	CCCTGAAATTTGACAACTCATACTTTCTTGACTACTGAAAGGGGAAATCTGAGGGCTT	615		
DB	762	CCCTTATCTTTGACAACTCTACTTCAACAGAGCTTGACAGGCTTGACAGAGAAGGCGTG	821		
QY	616	CTGAAGCTCCCTACTGATTAAGCATTTGTGATGATGCTGAAATTTGCAGCGTATGTGAG	675		
DB	822	CTTCAGTTCCCATCGATTAAGGCACACTGCTGTGATCCAGTTTGTGCAATTTGCA	881		
QY	676	CTTTATGCAAGAGATGAGGATGTTTCTTCAGAGGACTACCGTGATTCACACAAAATCT	735		
DB	882	AAGTATGCAAGAGACGAAAGACGCTTCTTCTGCTGACTATGCGGAAGCTCCTGAAAGCT	941		
QY	736	TCTGAACCTGGCTT 749			
DB	942	TCTGAACCTGGCTT 955			
RESULT 13					
LOCUS	AF411228	1138 bp	mRNA	linear	PLN 30-SEP-2001
DEFINITION	Artemium vulgare ascorbate peroxidase mRNA, complete cds.				
ACCESSION	AF411228				
VERSION	AF411228.1	GI:15808778			
KEYWORDS					

QY	540	TCGACGACTCGTGAGCCCTCGTAATTTGACAACATCATCTTCTTGACTGTGAAGG	599
Db	611	AGCCTGGACCCGCAACCCCTTATCTTCGACAACTTCTTACTGACCTCCTGATGG	670
QY	600	GGAAATCTGAGGGTCTTCTGAAAGCTCCCTACTGATGAAGGATGTTGGATGATCTGAAAT	659
Db	671	GGAGAAGGAAGGTCTTCTTCAAGTGGCCAGCCAAAGGTCGTCGACGACCCGGCCTT	730
QY	660	TCGACGCTATGTGGAGACTTTATGCAAGAGTATGAGATGTTTCTTCAGCACTACGCTGA	719
Db	721	CCGCCACTGTTGGACAATATATGCTGGCGGATGAGATGCTGCTTGTGCTACTACGCCGA	790
QY	720	ATCACAAAAAACTTCTGAACTGGGCTT	750
Db	791	GGCACACCTCAAGCTCTCTGAACTTGGATTTC	821
RESULT	14		
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LOCUS	ZMAPXG	1042 bp	mRNA linear PLN 01-DEC-1999
DEFINITION	Z.mays apx gene encoding cytosolic ascorbate peroxidase.		
ACCESSION	Z34934		
VERSION	Z34934.1	GI:600115	
KEYWORDS	cytosolic ascorbate peroxidase.		
SOURCE	Zea mays.		
ORGANISM	Zea mays.		
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	1 (bases 1 to 1042)		
TITLE	Van Breusegem, F., Villarroel, R., Van Montagu, M. and Inze, D.		
JOURNAL	Ascorbate peroxidase cDNA from maize		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 1042)		
TITLE	Van Breusegem, F.		
JOURNAL	Direct Submission		
FEATURES	Submitted (04-JUN-1994) Van Breusegem F., Labo voor Genetika, Universiteit Gent, Ledeganckstraat 35, Gent, Belgium, 9000		
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BASE COUNT	236 a	296 c	281 g
ORIGIN	970..975	229 t	
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Best Local Similarity	63.4%	Pred. No. 1.2e-62;	
Matches	467;	Conservative 0;	Mismatches 267; Indels 3; Gaps 1;
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Db	75	GTGAAGGCTACCCACGCGTGAACGAGCACTCAAGCGGCGTGCACAGGCCAAGCGT	134


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OY 76 GCCTTCCTGCTCCATCCGCTCCAGGAGATGCGCCGCCCATCATGCTCCGCTCCGATGC 135
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Db 135 AAGCTCCGGGGCTCATCGCCGAGAAAGATGGCCCGCTCATGCTCCGCTCCGATGC 194
OY 136 CATGATGCTGGACACTATGATGTGACACAAAGAACTGGTGGCAATGGTCAATAGA 195
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Db 195 CACTCCGTGGGCACTTCATGTGTGTACCAAAAACGGGGGCCCTTCGGCACCATAG 254
OY 196 TACGAGGAAGATACACCCATGCTCAAAATGCTGCTTAAAAATGGTATGATCTCTT 255
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Db 255 AACCCCGTAGAGACGCGACGCTGCACAGCCGGAATGGCAATGGCATAGGCTGCTA 314
OY 256 GAGCCATTAAAGCGAAGATCAAGATATACATATGCCAACCTTCATGACCTTGGCGGA 315
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Db 315 GAGCCATCAAGAGACAGTTCCTCATCTATCCCTAGCTGATCTTACAGCTTGGCTGA 374
OY 316 GTAGTTGACGTTGACATCCAGGGGGTCCAAACGTTGAGTTCACTCCCTGGAGACGTAT 375
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Db 375 GTGTGGGAGTGGAGTGAACCGGGGACCTGATGTCCCTCCACCTGGGAGGACGAGAC 434
OY 376 TCGTCAGTTTGTCCCGGTGAGAGCGCTTCTGATGCTAAGAAAGGTGACCAATCTA 435
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Db 435 AAGCTGAGCTTCACCGGAGGCGCTTCTGATGCCACCAAGGTTCTGAACCTC 494
OY 436 AGGACATCTTTT--ATGGAATGGGGTTAACAGACAAAGATATTGAGACTATCTGGG 492
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Db 495 AGGAGGTTTCTCCACACAGATGGTGTGAGGACGAGACATGTTGGCTTGTGGT 554
OY 493 GGGCAGACGCTGGGAAAGCGCATCTGAAAGGTGTGGTTGACGGTGCATGACTCGT 552
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Db 555 GGTCAACCCCTGGGAAGATGCCACAAGACAGGTCTGATTTAGAGGAGCTTGACCTC 614
OY 553 GACCTCTGAATTTTGACAACTATATCTTCTTGACCTACTGAGGAGGGAATCTGAGGT 612
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Db 615 AACCTTTGATCTTACCACTCTTACTTCAGAGAGCTTGTAGCGAGAGAAAGAGG 674
OY 613 CTTTGAAGCTCCCTACATATAAGCATGTGTGATGATCCTCAATTTGACACCTATGTG 672
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Db 735 GACAAATAGCAGGCGAGGAGCGCTTCTTGTGCTGACTACGCCGACGCTGAG 794
OY 733 CTTTCTGAAGCTTGCTT 749
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Db 795 CTTTCAAGATTGGATT 811

RESULT 15
LOCUS AF159627 1012 bp mRNA linear PLN 16-NOV-2001
DEFINITION Fragaria x ananassa cytosolic ascorbate peroxidase (APX) mRNA,
APX18 allele, complete cds.
ACCESSION AF159627
VERSION AF159627.1 GI:5257545
KEYWORDS
SOURCE
ORGANISM
Fragaria x ananassa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Rosoidae; Fragaria.
REFERENCE
AUTHORS Kim,I.J., Lee,B.H., Jo,J. and Chung,W.I.
TITLE Sequence variability of nine cytosolic ascorbate peroxidases in
polyloid strawberry
JOURNAL DNA Seq. 11 (6), 475-484 (2001)
MEDLINE 21554286
PUBMED 11696974
REFERENCE 2 (bases 1 to 1012)
AUTHORS Kim,I.J. and Chung,W.I.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Biological Sciences, Korea Advanced

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FEATURES             Institute of Science and Technology, 373-1 Kusong-dong, Yuseong-gu,
                      Taejeon 305-701, Korea
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BASE COUNT          233 a 241 c 252 g 286 t
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Best Local Similarity 62.8%; Pred No. 6.8e-62;
Matches 485; Conservative 0; Mismatches 282; Indels 5; Gaps 2;
OY 34 GTGAGCGCCAGTACCTGGCGCCAGTGCAGAGGCGCGGCCCTTCGTCCTCATC 93
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OY 94 GCCTCAAGGAGATCGCCGCCCATCATGCTCCGCTCGCATGCGATGATGCTGGACCTAT 153
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Db 126 GCCGAAAGAACTGCGCTCTCATGCTCCGCTGCTGATGACATGCTGCTGGAACCTAT 185
OY 154 GATGTAAACAAGAACTGGTGTGCAAAATGGTTCAATATAGATACGAGGAAGATACAC 213
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Db 186 GATGTAAACATTAAGACCGAGGCCCATTCGAGACCATATAGACAGTCGCTGAGCTCCT 245
OY 214 CATGTTCAAAATGCTGCTTAAATATGCTATTGATCTCTTGAAGCTATTAACGGAAG 273
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Db 246 CACGGCGCTTAACAATGATGCTTGCATTTGCTGACAGCTCTGAGGCGCATCAAGAGCAG 305
OY 274 CATCCAAAGATTTACATATCAGACCTTTCATCAAGCTTCCGCGAGTGGTGCATTAATGC 333
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Db 306 TTCCCTATTCTCTTACGCTGACCTTCTACCAAGTTGGGAGTTGCTGCTGTAGGTC 365
OY 334 ACCGGGGTCCAAACGTTGATCATCTCCTGGAAGACGATGCTCAGTTTGTCCCGCT 393
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Db 366 ACCGGTGAACCTGATGATTTCCATTTCCACCGAGAAAGAGAGAAACACCAACCAACCA 425
OY 394 GAAGAACGCCCTTCCTGATCTTAAGAAAGGTGACACCATCTAAGGAGACATCTT--TAT 450
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Db 426 GAAGGCCGCTTCTGATGATCTGGAAGGCTTCTGACCACTTGAAGGAAGTGTGGCAAA 485
OY 451 CGAATGGGTTTAACACAAAGATATTGATGACATATCTGGGGGGCACACCTGGGAAG 510
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Db 486 ACCATGGGTCTCAGCACGACGACATGTTGCTCTCTGCTGAGTGAACCTTGGGAAGG 545
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OY 571 AACTCATCTTCTTGAGCTACTGAAGGGGGAATCTGAGGGTCTTGAAGCTCCCTACT 630
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Db 606 AACTCATATTTACTGTGCTATTGATGAGAGAAAGGCTCTTCAAGTTCCAACT 665
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Db 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERSGFGAMTRDP 180
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AC Q39780;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
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DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ASCORBATE PEROXIDASE.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DELTAPINE 62;
RX MEDLINE=96351186; PubMed=8742335;
RA Burkemann J.R., Trelease R.N.;
RT "Ascorbate peroxidase. A prominent membrane protein in oilseed
RT glyoxysomes.";
RL Plant Physiol. 110:589-598(1996).
DR EMBL; U37060; AAB52954.1; -.
DR HSSP; P48534; IAPX.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase; 1.
DR PRINTS; PR00458; PEROXIDASE.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS00436; PEROXIDASE_2; 1.
DR KX Peroxidase.
SQ SEQUENCE 288 AA; 31942 MW; ADF15C705ED54C4E CRC64;

Query Match 82.8%; Score 1240.5; DB 10; Length 288;
Best Local Similarity 80.4%; Pred. No. 6.1e-94;
Matches 234; Conservative 26; Mismatches 28; Indels 3; Gaps 1;

QY 1 MAAPVDAEYLROVDARARAFRLIASKGAPIMLRILAMHDAAGTYDVMTRTGANGSIRY 60
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Db 241 ELGFTPRSSGPASTKSDYSTAVVLAOSAVGVAVAAVVIAAGTYLEASKRSK 291

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Q9XGS8 PRELIMINARY; PRT; 288 AA.
ID Q9XGS8;
AC Q9XGS8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)

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DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
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GN CMAPX.
OS Zantedeschia aethiopica (White calla lily).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Zantedeschia.
OX NCBI_TaxID=69721;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Lino-Neto T., Tavares R.M., Palme K., Pais M.S.S.;
RT "Expression of ascorbate peroxidase during senescence and regreening
RT of Zantedeschia aethiopica spathe.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF159254; AAD43334.1; -.
DR HSSP; P48534; IAPX.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase; 1.
DR PRINTS; PR00458; PEROXIDASE.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS00436; PEROXIDASE_2; 1.
DR KX Peroxidase; Oxidoreductase.
SQ SEQUENCE 288 AA; 31433 MW; 28BBBCFELL1CBFD63 CRC64;

Query Match 80.5%; Score 1205.5; DB 10; Length 288;
Best Local Similarity 78.0%; Pred. No. 4.6e-91;
Matches 227; Conservative 33; Mismatches 28; Indels 3; Gaps 1;

QY 1 MAAPVDAEYLROVDARARAFRLIASKGAPIMLRILAMHDAAGTYDVMTRTGANGSIRY 60
Db 1 MAAPVDAEYLKEVDKARDLRLILKNCAPIMLRILAMHDAAGTYDVTGTGPPNGSIRN 60
QY 61 EEEYTHGNSNAGLKIADLLEPIKAKHPKITTYADLHQLAGVAVAVETGGPTVEFIPGRDS 120
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QY 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERSGFGAMTRDP 180
Db 121 SVCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERSGFGAMTRDP 180
QY 121 NCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERSGFGAMTRDP 180
Db 121 NCPREGRLPDAAKGAAPHLRDLFYRMGLTDKDIYALSGSHLKAHPERSGFGAMTRDP 180
QY 181 LKFDSNYFLELLKGSEGLLKLPTDKALLDDPEFRFVELYAKDEDFEFKDYESHKKLS 240
Db 181 LKFDSNYFLELLKGSEGLLKLPTDKALLDDPEFRFVELYAKDEDFEFKDYESHKKLS 240
QY 241 ELGFTPRSSGPASTKSDYSTAVVLAOSAVGVAVAAVVIAAGTYLEASKRSK 291
Db 241 ELGFT---SPKSASKDAHTSILLAGNSAVGVAVAAVVIAAGTYLEASKRSK 288

RESULT 4
Q948P1 PRELIMINARY; PRT; 286 AA.
ID Q948P1;
AC Q948P1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PEROXISOMAL ASCORBATE PEROXIDASE.
GN Cucurbita sp. cv. Kurokawa Amakuri.
OS Cucurbita sp. cv. Kurokawa Amakuri.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=170542;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. KUROKAWA AMAKURI;
RX MEDLINE=21109356; PubMed=11158440;
RA Nito K., Yamaguchi K., Kondo M., Hayashi M., Nishimura M.;
RT "Pumpkin peroxisomal ascorbate peroxidase is localized on peroxisomal
RT membranes and unknown membranous structures.";
RL Plant Cell Physiol. 42:20-27(2001).
DR EMBL; AB070626; BAB64351.1; -.

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KM Peroxidase. 286 AA; 31562 MW; 4BC6EC7997F012C0 CRC64;
 SQ SEQUENCE
 Query Match 79.4%; Score 1189.5; DB 10; Length 286;
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 Matches 225; Conservative 28; Mismatches 33; Indels 5; Gaps 1;
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 DB 1 MALPVDAEYLKKEIKARLRLALINRNCAPIMRLAMWHDAGTYDVNTRTGANGSTRY 60
 QY 61 EEEYTHGNSAGIKIALIDLEPIKAKHPKITYADLHQLAGVAVVEYTGPTVEFIPGRDS 120
 DB 61 QEEYTHGNSAGIKIALIDLEPIKAKHPKITYADLHQLAGVAVVEYTGPTVEFIPGRDS 120
 QY 121 SVPREGRLPDAKKAPHLRDIFYRMGLTQKDIVALSGHSLGKAKHPERSGFDGAMTRDP 180
 DB 121 RISPREGRLPDAKKAPHLRDIFYRMGLTQKDIVALSGHSLGKAKHPERSGFDGAMTRDP 180
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 DB 241 ELGFTPRSSGPASTKSDVSTAVVLAQSAAGVAAVYAGLYEASRSK 291
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 AC 042564;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ASCORBATE PEROXIDASE (EC 1.11.1.11) (L-ASCORBATE PEROXIDASE).
 GN APX OR APX3 OR M4E13.60 OR AT4G35000.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLOMBIA;
 RA Jespersen H.M., Kirsgaard I.V.H., Ostergaard L., Wejlander K.G.;
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Karpinski S., Escobar C., Karpinski B., Creissen G., Mullineaux P.;
 RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97435981; PubMed=9290648;
 RA Zhang H., Wang J., Nickel U., Allen R.D., Goodman H.M.;
 RT Cloning and expression of an Arabidopsis gene encoding a putative
 RT peroxisomal ascorbate peroxidase.";
 RL Plant Mol. Biol. 34:967-971(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Zhang H., Wang J., Nickel U., Allen R.D., Goodman H.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Purnelle B., Boutry M., Goffeau A., Hohlsel J., Mewes H.W.,
 RA Mayer K., Schueller C.; to the EMBL/GenBank/DBJ databases.
 RN Submitted (MAR-1998)
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.

RA Purnelle B., Boutry M., Goffeau A., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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 DR EMBL; U69138; AAB71493.1; -;
 DR EMBL; X98003; CA66640.1; -;
 DR EMBL; X98276; CA66926.1; -;
 DR EMBL; AL022023; CA11765.1; -;
 DR EMBL; AL161586; CAB80217.1; -;
 DR HSSP; P48534; IAPX.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF00141; peroxidase.1.
 DR PRINTS; PR00458; PEROXIDASE.
 DR PROSITE; PS00435; PEROXIDASE_1; 1.
 DR PROSITE; PS00436; PEROXIDASE_2; 1.
 KM Peroxidase; Oxidoreductase.
 SQ SEQUENCE 287 AA; 31572 MW; B348E74BA34115DE CRC64;
 Query Match 79.0%; Score 1183; DB 10; Length 287;
 Best Local Similarity 75.9%; Pred. No. 3.2e-89;
 Matches 221; Conservative 34; Mismatches 32; Indels 4; Gaps 1;
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 DB 1 MAPVDAEYLKKEIKARLRLALINRNCAPIMRLAMWHDAGTYDQAKGTGPGNGSTRN 60
 QY 61 EEEYTHGNSAGIKIALIDLEPIKAKHPKITYADLHQLAGVAVVEYTGPTVEFIPGRDS 120
 DB 61 EEEYTHGNSAGIKIALIDLEPIKAKHPKITYADLHQLAGVAVVEYTGPTVEFIPGRDS 120
 QY 121 SVPREGRLPDAKKAPHLRDIFYRMGLTQKDIVALSGHSLGKAKHPERSGFDGAMTRDP 180
 DB 121 SVPREGRLPDAKKAPHLRDIFYRMGLTQKDIVALSGHSLGKAKHPERSGFDGAMTRDP 180
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 DB 121 NVCPEGRRLPDAKQFOHRLDFYRMGLTQKDIVALSGHSLGKAKHPERSGFDGAMTRDP 180
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 DB 181 LKFDNSYFELLKGESEGLIKLPTDKALIDDEPRFRVVELYAKDDVPEFKDYAESHKKLS 240
 QY 241 ELGFTPRSSGPASTKSDVSTAVVLAQSAAGVAAVYAGLYEASRSK 291
 DB 241 ELGFTPRSSGPASTKSDVSTAVVLAQSAAGVAAVYAGLYEASRSK 291
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 AC 081810;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ASCORBATE PEROXIDASE.
 GN APXIII.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLOMBIA;
 RA Escobar C., Bradley D.J., Puente P., Harberd N., Creissen G.P.,
 RA Mullineaux P.M.;
 RT "Ascorbate peroxidase III gene from Arabidopsis thaliana is regulated
 RT by light and development.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ006030; CAA06823.1; -;
 DR HSSP; P48534; IAPX.
 DR InterPro: IPR002016; Peroxidase.

DR Pfam: PF00141; peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
KW Peroxidase.
SQ SEQUENCE 287 AA: 31585 MW; 05BC1E229FA0BB4 CRC64;

[illegible]

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DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)			
DT	01-DEC-2001 (TREMblrel. 19, Last annotation update)			
DE	ASCORBATE PEROXIDASE 2.			
GN	APX2.			
OS	Glycine max (Soybean).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.			
OX	NCBI_TaxID=3847;			
RP	SEQUENCE FROM N.A.			
RA	Turan F.J., McMahon M.B., Caldwell C.R.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U05634; AAB0121.1; -.			
DR	HSSP; P48534; IAPX.			
DR	InterPro; IPR002016; Peroxidase.			
DR	Pfam; PF00141; peroxidase.1.			
DR	PRINTS; PR00458; PEROXIDASE.			
DR	PROSITE; PS00435; PEROXIDASE_1; 1.			
DR	PROSITE; PS00436; PEROXIDASE_2; 1.			
KW	Peroxidase.			
SD	SEQUENCE 250 AA; 27139 MW; 55E5671A914D9E31 CRC64;			
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	Matches 156; Conservative 32; Mismatches 51; Indels 1; Gaps			
QY	4 PVYDAEYLROYDARARAFRALIASGCAPIMLRLAMHDAGTYDVNTRTGANGSIRYEE 63			
DB	6 PTVADYOKAEKAEKKKRGFIARCRAPLMLRLAMSHSAGTYDVSSKGTGPFGRHKPSE 65			
QY	64 YTHSSNGKLKAIIDLLEPIRKHKHTIYADLHOLAGYAAVYVNGGPFYERIPGRDSSVC 125			
DB	66 LAHANNGLDVAIVLLEFLKAEPIPLYADYQYLAGVAAEVYTGPEYPRPGRGREDPEP 125			
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QY	183 FDNISFYLELKGSEGLKLPDTKALLDDPEFRYVELYAKDEVFFKDYAESKKSSEL 243			
DB	186 FDNISFYLELKGSEGLKLPDPSKALLSDPYFRPLVERKASDEDADFADYAEAHOKLSEL 243			
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DB	246 GF 247			
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AC	042941;			
DT	01-NOV-1996 (TREMblrel. 01, Created)			
DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)			
DT	01-DEC-2001 (TREMblrel. 19, Last annotation update)			
DE	ASCORBATE PEROXIDASE (EC 1.11.1.11).			
GN	APX.			
OS	Nicotiana tabacum (Common tobacco).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; eusterid 1; Solanales; Solanaceae; Nicotiana.			
OX	NCBI_TaxID=1097;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=XANTH; TISSUE=LEAF;			
RX	MEDLINE=95334507; PubMed=7610178;			
RT	Ottav B.L., Ellis B.E.;			
TL	"Isolation of a cDNA encoding cytosolic ascorbate peroxidase in tobacco.";			
PL	Plant Physiol. 108:839-840(1995).			

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OM protein - protein search, using sw model

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Run on:      October 23, 2002, 13:56:19 ; Search time 32 Seconds
              (without alignments)
              1010.077 Million cell updates/sec
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
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Post-processing:  Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1183	79.0	287	21	AA609460	Arabidopsis thaliana
2	1183	79.0	287	21	AA643316	Arabidopsis thaliana
3	1152	76.9	287	21	AAV77933	Arabidopsis thaliana
4	1061	70.8	254	21	AA609461	Arabidopsis thaliana
5	1061	70.8	254	21	AA643317	Arabidopsis thaliana
6	818.5	54.6	250	21	AA609702	Arabidopsis thaliana
7	818.5	54.6	250	21	AA618805	Arabidopsis thaliana
8	818.5	54.6	250	21	AA626453	Arabidopsis thaliana
9	818.5	54.6	250	21	AA643523	Arabidopsis thaliana
10	818.5	54.6	250	21	AA645582	Arabidopsis thaliana
11	818.5	54.6	250	21	AA645585	Arabidopsis thaliana

12	818.5	54.6	250	21	AAAG55589	Arabidopsis thaliana
13	818.5	54.6	254	21	AAAG343522	Arabidopsis thaliana
14	818.5	54.6	297	21	AAAG26452	Arabidopsis thaliana
15	818.5	54.6	297	21	AAAG45588	Arabidopsis thaliana
16	737.5	49.2	215	21	AAAG09703	Arabidopsis thaliana
17	737.5	49.2	215	21	AAAG16806	Arabidopsis thaliana
18	737.5	49.2	215	21	AAAG6454	Arabidopsis thaliana
19	737.5	49.2	215	21	AAAG3524	Arabidopsis thaliana
20	737.5	49.2	215	21	AAAG45583	Arabidopsis thaliana
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22	737.5	49.2	215	21	AAAG45590	Arabidopsis thaliana
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24	650.5	43.4	191	21	AAAG16807	Arabidopsis thaliana
25	650.5	43.4	191	21	AAAG45584	Arabidopsis thaliana
26	650.5	43.4	191	21	AAAG45587	Arabidopsis thaliana
27	640.5	42.8	354	21	AAAG44544	Arabidopsis thaliana
28	640.5	42.8	426	21	AAAG44543	Arabidopsis thaliana
29	640.5	42.8	452	21	AAAG44542	Arabidopsis thaliana
30	631.5	42.2	348	21	AAAG05527	Arabidopsis thaliana
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32	631.5	42.2	353	21	AAAG05526	Arabidopsis thaliana
33	631.5	42.2	372	21	AAAG52696	Arabidopsis thaliana
34	629.5	42.0	347	21	AAAG24604	Arabidopsis thaliana
35	629.5	42.0	353	21	AAAG24603	Arabidopsis thaliana
36	484	32.3	122	17	AAAG89746	AFT-1 interacting
37	477.5	31.9	182	21	AAAG43945	Arabidopsis thaliana
38	405	27.0	134	21	AAAG16113	Arabidopsis thaliana
39	405	27.0	136	21	AAAG25637	Arabidopsis thaliana
40	405	27.0	140	21	AAAG25636	Arabidopsis thaliana
41	405	27.0	164	21	AAAG16112	Arabidopsis thaliana
42	377	25.2	238	21	AAAG33207	Arabidopsis thaliana
43	374	25.0	102	21	AAAG33207	Zea mays protein F
44	373.5	24.9	366	21	AAAG1748	Arabidopsis thaliana
45	373.5	24.9	366	21	AAAG1747	Arabidopsis thaliana

ALIGNMENTS

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XX	17-OCT-2000 (first entry)
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 7405
DE	Protein identification; signal transduction pathway; m
XX	hybridisation assay; genetic mapping; gene expression
KW	termination sequence.
KW	Arabidopsis thaliana.
OS	Arabidopsis thaliana.
XX	EP1033405-A2.
PN	06-SEP-2000.
XX	06-SEP-2000.
PD	25-FEB-2000; 2000EP-0301439.
XX	25-FEB-1999; 99US-0121825.
XX	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0128234.
PR	06-APR-1999; 99US-0128714.
PR	08-APR-1999; 99US-0128845.
PR	16-APR-1999; 99US-0130077.
PR	19-APR-1999; 99US-0130449.
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PR 23-APR-1999; 99US-0130510.
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PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
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PR 04-JUN-1999; 99US-0137502.
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PR 17-JUN-1999; 99US-0139492.
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PR 21-JUN-1999; 99US-0139817.
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PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141847.
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PR 02-JUL-1999; 99US-0142055.
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PR	28-OCT-1999	99US-01613623
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PR	28-OCT-1999	99US-01621143

Query Match	79.0%;	Score 1183;	DB 21;	Length 287;
Best Local Similarity	75.9%;	Pred. No. 1.2e-117;		
Matches 221;	Conservative 34;	Mismatches 32;	Indels 4;	Gaps 1;

[illegible]

RESULT 3
AA777933
ID AA777933 standard; protein; 287 AA.
XX
XX
AC AA777933;
XX
XX 14-JUN-2000 (first entry)
DT
XX
DE A. thaliana environmental stress tolerance related protein.
XX
XX
KW Environmental stress; plant; transgenic plant; anaerobic; flooding; cold;
dehydration; drought; heat stress; salinity; osmotolerance.
XX
XX
OS Arabidopsis thaliana.
XX
XX
PN W0200008187-A2.

XX 17-FEB-2000.
PD 04-AUG-1999; 99WO-EP05652.
XX 04-AUG-1998; 98EP-0202634.
PR (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX Lee JH, Verbruggen N;
PI WPI: 2000-205726/18.
XX N-PSDB; AA298313.
PT Isolation of polynucleic acids useful for producing transgenic plant by
XX isolating genes involved in tolerance to environmental stress
PS Claim 12; Page 112-115; 312pp; English.
XX The invention relates to isolation of coding sequences and/or genes
CC involved in tolerance to environmental stress in plants. The sequences
CC (AA298305-298365) are useful for producing a transgenic plant having
CC enhanced tolerance or resistance to environmental stress conditions such
CC as anaerobic, flooding, cold, dehydration, drought, heat stress or
CC salinity. This is useful for producing improved yield, growth,
CC development and productivity under environmental stress conditions, and
CC also provides growth of crops in areas where they cannot grow without
CC the induced osmotolerance. Sequences AA27925-984 represent polypeptide
CC sequences from A. thaliana that are encoded by the genes involved in
CC environmental stress tolerance.
XX Sequence 287 AA;
SQ
Query Match 76.9%; Score 1152; DB 21; Length 287;
Best Local Similarity 75.0%; Pred. No. 2.4e-114;
Matches 219; Conservative 34; Mismatches 33; Indels 6; Gaps 3;
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DB 1 MAAPVDAEYLRQVDRARRAFRALIASKCAPIMLRMLAMHDAGTYVTRTGANGSIRN 60
QY 61 EEEYHSGNAGIKTAIDLEPIKAKHFKITTAADLHQLAGVAVEYTGPTVEFIPGRDS 120
DB 61 EEEYHSGNAGIKTAIDLEPIKAKHFKITTAADLHQLAGVAVEYTGPTVEFIPGRDS 120
QY 121 SVCPREGRLPPAKKGAPHLRDIFYRMGLTDKDIYALSGHSLGKAHPRSGFDGAWTRDP 180
DB 121 NVCPREGRLPPAKKGAPHLRDIFYRMGLTDKDIYALSGHSLGKAHPRSGFDGAWTRDP 180
QY 181 LKFDNSYFL-ELLNGESGLLKLPTDKALLDPEFRRYVELYAKDEDEVFPDYAESHKRL 239
DB 181 LKFDNSYFL-ELLNGESGLLKLPTDKALLDPEFRRYVELYAKDEDEVFPDYAESHKRL 239
QY 240 SELGTPSSGSPASTKSYSTAVYLAOSAGVAAVAAVINGLYLEAKRSK 291
DB 240 SELGTPSSGSPASTKSYSTAVYLAOSAGVAAVAAVINGLYLEAKRSK 291
RESULT 4
AAC09461
ID AAC09461 standard; Protein: 254 AA.
XX AAC09461;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 7406.
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.

XX EP1033405-A2.
PN 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
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Best Local Similarity 77.1%; Pred. No. 1e-104;
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DB 1 MRLAHMDAGTYDAOSKTGPNGSIRNEEHTHGANSGLKTALDCEGVAKAKHPRITYAD 60
QY 94 LHOLAGVAVAEVYTGPTVEFIPGRDSSVCPREGRILPPAKKGAPLHRDIFFRMGITDKDI 153
DB 61 LVOLAGVAVAEVYTGPDYIFVYPRGRDSSVCPREGRILPPAKKGFOLHRVFRMGISDKDI 120
QY 154 VALSGSHSLGKAHPERSGFGDGAWTRDPLKEDNSYFLELLKGESEGLKLPDKALLDPE 213
DB 121 VALSGHFTLGRAHPERSGFGDGPWQEPKFDNSYFVEILLKGESEGLKLPDKTLLDPE 180
QY 214 FRRYVELYAKDDVFPKDAESHKRLSELGTFPRSSGASRSDVSTVAVAQSAVGVAV 273
DB 181 FRRYVELYAKDDVFPKDAESHKRLSELGTFPRSSGASRSDVSTVAVAQSAVGVAV 236
QY 274 AAAYVAGTYEASKRSK 291
DB 237 AAAYVAGTYEIRKKRM 254

RESULT 5
AAG43317
ID AAG43317 standard; Protein; 254 AA.
XX
AC AAG43317;
XX

DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 54128.
DE
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
PN EPI033405-A2.
PD
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 29-MAR-1999; 99US-0126785.
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PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
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DB 1 MLRLAMHDAGTYDQSKGPGNGSIRNEEHTHGANSGLIKTALDCEGAKAKHPKITTYAD 60
QY 94 LHOAGVAVAVTGGPTVEFLIPGRDSSVCPREGRLPDAKCAPRLDITFYMGJLTDKI 153
DB 61 LYQLAGVAAVAVTGGPDVFPVGRKDSNVCPREGRLPDAKQGFOLRDVFMGLSDKDI 120
QY 154 VALSGSHLGAHBERSGFDGAWTRDPLKFDNSYFLELLKGESEGLIKLPTDKALLDPE 213
DB 121 VALSGHHTLGAHBERSGFDGAWTRDPLKFDNSYFLELLKGESEGLIKLPTDKALLDPE 180
QY 214 FRRYVELYADEDEVFKDYASHKLSLGLFTPRSSGPASTKSDYSTAVVLAQSAVGVAV 273
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XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
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XX termination sequence.
OS Arabidopsis thaliana.
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Best local similarity 63.6%; Pred. No. 7.9e-79; Indels 1; Gaps 1;

Matches 154; Conservative 32; Mismatches 55; Indels 1; Gaps 1;

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| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
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QY 124 PREGPLPAKKGAPHLRIEYR-MGLTDXDVALSGSGSLKAPEREGFGGANTROPDK 182
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
D 126 PREGPLPATGCHLRVFKOMGLSDKDIVALSGAHTTGRCHDRSGEGGAMTINPLI 185
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 183 FDNSTFLEILGSEEGGLKLPDTRKALDDPFRFRRVELYAKDEVEFFDYAESHKUSEL 242
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
D 186 FDNSTFKLLSGEKEGLQLVSDKALLDDPVFRPLVEKYADEAFADYAEAMKUSSEL 245
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RESULT: 13

AAG43522 standard; Protein; 254 AA.

AAG43522;

18-OCT-2000 (first entry)

XX XX Arabidopsis thaliana protein fragment SEQ ID NO: 54409.
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XX XX Protein identification; signal transduction pathway; metabolic pathway;
KW KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW KW termination sequence.
XX XX Arabidopsis thaliana.
OS OS
XX XX EPI033405-A2.
PN PN
XX XX
PD PD
XX XX 06-SEP-2000.
XX XX
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PR PR 09-MAR-1999; 99US-0123548.
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PR PR 25-MAR-1999; 99US-0126264.
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KM hydridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
OS Arabidopsis thaliana.
XX
PM EPI033405-A2.
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QY	64	YTHSSNMGKLAIDLLEPIKAKHKITYADLHQAGVAAVEVGGPVEETIPGRDSSVC	133		
DB	113	QAHGANSQIHIALRLDPIRQPTLISPADFHQAGVAAVEVGGPDIPIPHGREDKPP	172		
QY	124	PREGRLPAKAGAPHLRIDFTR-MGLTDDKDIVALSGSHLGAKHPERSGFDGANTRPDK	192		

Db	173	PREGULPDATKCDHLRDVFAKQMSDKDIALVALSGAHTTLCGRCHKDKDSGFEQANTSNPLI	232		
Qy	183	FDNYSFLELLKGESEGLLKLPTRKALLDDPEFRRYVELYAKDEVEFFKDYAESHRKLSL	242		
Db	233	FDNYSFKEILLSEKRGILLQIVSDKALLDDPVFRPLVEKRYADEDAFADYAEAHMKLSL	292		
Qy	243	GF 244			
Db	293	GF 294			
RESULT 15					
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XX	AAG45588 standard; Protein: 297 AA.				
XX	AAG45588;				
AC					
XX					
DT	18-OCT-2000 (first entry)				
XX					
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 57253.				
XX					
KM	Protein identification: signal transduction pathway; metabolic pathway;				
KM	hybridisation assay; genetic mapping; gene expression control; promoter.				
XX					
OS	Arabidopsis thaliana.				
XX					
PN	EPI033405-A2.				
XX					
PD	06-SEP-2000.				
XX					
PF	25-FEB-2000; 2000EP-0301439.				
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PR	25-FEB-1999;	99US-0121825.			
PR	05-MAR-1999;	99US-0123180.			
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PR	23-MAR-1999;	99US-0125788.			
PR	25-MAR-1999;	99US-0126264.			
PR	29-MAR-1999;	99US-0126785.			
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PR	06-APR-1999;	99US-0128234.			
PR	08-APR-1999;	99US-0128714.			
PR	16-APR-1999;	99US-0129845.			
PR	19-APR-1999;	99US-0130077.			
PR	21-APR-1999;	99US-0130449.			
PR	23-APR-1999;	99US-0130510.			
PR	23-APR-1999;	99US-0130891.			
PR	28-APR-1999;	99US-0131449.			
PR	30-APR-1999;	99US-0132048.			
PR	30-APR-1999;	99US-0132407.			
PR	04-MAY-1999;	99US-0132484.			
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PR	06-MAY-1999;	99US-0132486.			
PR	07-MAY-1999;	99US-0132487.			
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PR	27-MAY-1999;	99US-0136392.			
PR	28-MAY-1999;	99US-0136782.			
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PR	03-JUN-1999;	99US-0137528.			
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PR 01-JUL-1999; 99US-0141842.
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PR 06-JUL-1999; 99US-0142390.
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PR 02-AUG-1999; 99US-0146386.
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PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
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PR 09-AUG-1999; 99US-0147493.

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PR 18-AUG-1999; 99US-0149426.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154479.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 54.6%; Score 818.5; DB 21; Length 297;
Best Local Similarity 63.6%; Pred. No. 1e-78;
Matches 154; Conservative 32; Mismatches 55; Indels 1; Gaps 1;
QY 4 PYYDAEYLRQVDRARRPALIASKGCAPIMLRMLAHWDAGTYDVNTRFGGANGSIRYEEE 63

Db 53 PTVSEDYKKAVERCKRRKLRGLIAEKNCAPIWRIAMHSAGTFDQOSRTGPFGTMRPDAE 112
QY 64 YTHGSNAGLKIADLLEPIKAKHPKITTYADLHOLAGVAVETGGPTVEFIPGRDSSVC 123
Db 113 QAHGANSGIHIALRLDPIREQPPTISFADFRLAGVAVETGGPDIPFHPGRDCKPQ 172
QY 124 PREGRLPDAKKGAHRLDIFYR-MGLTDKDIVALSGGHSIGKAHPERSGFGAMTRDPLK 182
Db 173 PEGRLPDATKGGCDHLDVFAKOMGLSDKDIVALSGAHTLGRCHKDRSGFEGAMTSNPLI 232
QY 183 FDNSTFLELLKGSBGLKLPMDKALDDPEFRRYVELYAKDEVDPEKDYAESHKLSL 242
Db 233 FDNSTFKELLSGKEBGLQLVSDKALDDPEFRPLVEKYADEDAEPADYAEAHMKLSL 292
QY 243 GF 244
Db 293 GF 294

Search completed: October 23, 2002, 13:58:44
Job time : 34 secs

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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:56:19 ; Search time 14 Seconds

(without alignments)
804.814 Million cell updates/sec

Title: US-09-870-501-1

Perfect score: 1498
Sequence: 1 MAAPVDAEYLROYDRARRA.....AVAAVVIAGLYEASKRSK 291

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	818.5	54.6	249	1	APX1_ARATH
2	802.5	53.6	249	1	APX1_PEA
3	457	30.5	361	1	CCPR_YEAST
4	317	21.2	735	1	CATB_BACST
5	294	19.6	737	1	CATB_YERPE
6	280.5	18.7	731	1	CATB_HALMA
7	276.5	18.5	720	1	CATB_HALNI
8	272.5	18.2	749	1	CATB_LEGNP
9	265	17.7	741	1	CATB_ARCFU
10	257	17.2	726	1	CATB_ECOLI
11	254.5	17.0	726	1	CATB_SALTY
12	254	17.0	740	1	CATB_MYCOB
13	254	17.0	740	1	CATB_MYCMU
14	245.5	16.4	739	1	CATB_MYCSM
15	244.5	16.3	737	1	CATB_CAVCR
16	235.5	15.7	740	1	CATB_STRRE
17	232	15.5	752	1	CAT1_MYCFO
18	231.5	15.5	740	1	CATB_STRRO
19	226.5	15.9	746	1	CATB_MYCIT
20	208.5	13.9	349	1	TL29_ARATH
21	201.5	13.5	378	1	PEM1_PHACH
22	201.5	13.5	382	1	PEM4_PHACH
23	201	13.4	345	1	TL29_LYCES
24	199.5	13.3	576	1	CATB_RHOCA
25	187	12.5	292	1	PER2_CUSCA
26	171.5	11.4	347	1	PER2_ARMARU
27	171	11.4	322	1	PERX_ARMARU
28	170	11.3	364	1	PERX_ARMARU
29	167.5	11.2	363	1	PERX_ARMARU
30	167.5	11.2	305	1	PERX_ARMARU
31	166.5	11.1	330	1	PER2_ARMARU
32	164	10.9	296	1	PERX_ARMARU
33	162.5	10.8	332	1	PERX_ARMARU

34	161	10.7	316	1	PER1_ARMARU
35	160.5	10.7	353	1	PERA_ARMARU
36	160	10.7	349	1	PERE_ARMARU
37	158	10.5	324	1	PERX_ARMARU
38	158	10.5	326	1	PER1_ARMARU
39	155.5	10.4	312	1	PER1_ARMARU
40	155.5	10.4	354	1	PER2_ARMARU
41	151.5	10.1	351	1	PERB_ARMARU
42	149	9.9	372	1	PERB_ARMARU
43	145	9.7	372	1	PERB_ARMARU
44	144.5	9.6	314	1	PER2_ARMARU
45	137	9.1	349	1	PER3_ARMARU

ALIGNMENTS

RESULT 1	ID	APX1_ARATH	STANDARD:	PRT:	249 AA.
AC	005431;				
DT	01-FEB-1995 (Rel. 31, Created)				
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	L-ascorbate peroxidase, cytosolic (EC 1.11.1.11) (Ap).				
GN	APX1 OR AP1G07890 OR P24B9.2.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OC	Eurosids II; Brassicales; Brassicaceae; Arabidopsids.				
OX	NCBI_TaxID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV, COLUMBIA;				
RX	MEDLINE=93138095; PubMed=8422923;				
RA	Kudo A., Saij H., Tanaka K., Kondo N.;				
RT	"Genomic DNA structure of a gene encoding cytosolic ascorbate				
RT	peroxidase from Arabidopsids thaliana.";				
RL	FEBS Lett. 315:313-317(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 1-16.				
RC	STRAIN=CV, COLUMBIA; TISSUE=Leaf;				
RX	MEDLINE=92216045; PubMed=1558944;				
RA	Kudo A., Saij H., Tanaka K., Tanaka K., Kondo N.;				
RT	"Cloning and sequencing of a cDNA encoding ascorbate peroxidase from				
RT	Arabidopsids thaliana.";				
RL	Plant Mol. Biol. 18:691-701(1992).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV, COLUMBIA;				
RA	Tremousaygue D., Bardet C., Dabos P., Regad F., Pelase F.,				
RA	Lescur B.;				
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV, COLUMBIA;				
RA	MEDLINE=21016719; PubMed=11130712;				
RA	Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,				
RA	White O., Alonso J., Atafati H., Araujo R., Bowman C.L., Brooks S.Y.,				
RA	Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,				
RA	Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,				
RA	Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,				
RA	Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizlar L.,				
RA	Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,				
RA	Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,				
RA	Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,				
RA	Liu X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,				
RA	Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,				
RA	Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,				
RA	Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,				
RA	Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,				
RA	Uttterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,				
RA	Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;				

"Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana.";
RL Nature 406:816-820(2000).
CC -1- FUNCTION: PLAYS A KEY ROLE IN HYDROGEN PEROXIDE REMOVAL IN
CC THE CHLOROPLASTS AND CYTOSOL OF HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: L-ascorbate + H(2)O(2) -> dehydroascorbate + 2
CC H(2)O.
CC -1- COFACTOR: HEME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- INDUCTION: BY STRESS.
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. CYTOCHROME C
CC PEROXIDASE SUBFAMILY.
CC -1- CAUTION: REF.2 SEQUENCE IS INCORRECT.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL: D14442; BAA0334.1; -
CC EMBL: X59600; CAA42168.1; -
CC EMBL: U63815; AAB07880.1; -
CC EMBL: AC007583; AAF75066.1; -
CC PIR: S28856; S28856.
CC HSSP: P48534; IAPX.
CC SWISS-2DPAGE: Q05431; ARATH.
CC InterPro: IPR002016; Peroxidase.
CC Pfam: PF00141; peroxidase.1.
CC PRINTS: PR00458; PEROXIDASE.
CC PROSITE: PS00435; PEROXIDASE_1; 1.
CC PROSITE: PS00436; PEROXIDASE_2; 1.
CC Oxidoreductase; Peroxidase; Hydrogen peroxide; Heme.
CC INT_MET 0 0
CC FT ACT_SITE 37 37 BY SIMILARITY.
CC FT ACT_SITE 41 41 DISTAL HISTIDINE (BY SIMILARITY).
CC FT ACT_SITE 162 162 PROXIMAL HISTIDINE (HEME AXIAL LIGAND)
CC (BY SIMILARITY).
CC FT SEQUENCE 249 AA; 27430 MM; 33B70FD85B075A6C CRC64;
SQ
Query Match 54.6%; Score 818.5; DB 1; Length 249;
Best Local Similarity 63.6%; Pred. No. 9.4e-63;
Matches 152; Conservative 32; Mismatches 55; Indels 1; Gaps 1;
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CC 4 PYDAEYLKQVDRARRARALIAKGCAPIMRLAMWDAGTYVNTRTGANGSIRYEE 63
CC | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
CC 5 PTVSSEDYKKAKEKRRKRLGLIAEKNCAPINWRLAMHSAGTDCQSRGCGPGTIRFDAE 64
CC | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
CC 64 YTHGSNGLKTAIDLEPIKAKHPKITYADLHQLGAVVAEVTGGPTVEFIPIGRDSSVC 123
CC | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
CC 65 QAHGANSIGIHRLRLDPIREQFPIISFADFHLQAGVVAEVTGGPDIPFHGRDQPPQ 124
CC | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
CC 124 PREGRLDKAGAHRLDIETFR-MGLTMDKDYALSSGHSILGAHBERSGFOCAWTRDPLK 182
CC | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
CC 125 PPEGRLEDPARKGCHLRVFAKMGSLKSDYALSGAHTLGCCHDRSGFEGAWTSNPLI 184
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CC 183 FDNYSFLELLKGESEGLKLTPTKALDDPEFRYVELYAKDEDEVFFDYAESHKLSL 242
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CC 243 GF 244
CC | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
CC 245 GF 246
CC | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
CC DB 245 GF 246
CC | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
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AC P48534;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 16-OCT-2001 (rel. 40, Last annotation update)
DE L-ascorbate peroxidase, cytosolic (EC 1.11.1.11) (AP).
GN APX1 OR APX1.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxId=3888;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LITTLE MARVEL; TISSUE=leaf;
RX MEDLINE=92006636; PubMed=1915856;
RA Mittler R., Zilinskas B.A.;
RT "Molecular cloning and nucleotide sequence analysis of a cDNA
RT encoding pea cytosolic ascorbate peroxidase.";
RL FEBS Lett. 289:257-259(1991).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LITTLE MARVEL;
RX MEDLINE=93016138; PubMed=1400489;
RA Mittler R., Zilinskas B.A.;
RT "Molecular cloning and characterization of a gene encoding pea
RT cytosolic ascorbate peroxidase.";
RL J. Biol. Chem. 267:21802-21807(1992).
RN (3)
RP ERRATUM.
RA Mittler R., Zilinskas B.A.;
RL J. Biol. Chem. 268:4568-4568(1993).
RN (4)
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA Patterson W.R., Poulos T.L.;
RL Submitted (Feb-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLAYS A KEY ROLE IN HYDROGEN PEROXIDE REMOVAL IN
CC THE CHLOROPLASTS AND CYTOSOL OF HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: L-ascorbate + H(2)O(2) -> dehydroascorbate + 2
CC H(2)O.
CC -1- COFACTOR: HEME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- INDUCTION: BY STRESS.
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. CYTOCHROME C
CC PEROXIDASE SUBFAMILY.
CC
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CC
CC EMBL: M93051; AAA33645.1; -
CC EMBL: X62077; CAA43992.1; -
CC PDB: IAPX; 08-MAR-96.
CC InterPro: IPR002016; Peroxidase.
CC Pfam: PF00141; peroxidase.1.
CC PRINTS: PR00458; PEROXIDASE.
CC PROSITE: PS00435; PEROXIDASE_1; 1.
CC PROSITE: PS00436; PEROXIDASE_2; 1.
CC Oxidoreductase; Peroxidase; Hydrogen peroxide; Heme; 3D-structure.
CC INT_MET 0 0
CC FT ACT_SITE 37 37 BY SIMILARITY.
CC FT ACT_SITE 41 41 DISTAL HISTIDINE (BY SIMILARITY).
CC FT ACT_SITE 162 162 PROXIMAL HISTIDINE (HEME AXIAL LIGAND)
CC (BY SIMILARITY).
CC FT SEQUENCE 249 AA; 27061 MM; 6F43396D0A38442C CRC64;
SQ
Query Match 53.6%; Score 802.5; DB 1; Length 249;
Best Local Similarity 62.8%; Pred. No. 2.2e-61;
Matches 152; Conservative 34; Mismatches 55; Indels 1; Gaps 1;
CC
CC 4 PYDAEYLKQVDRARRARALIAKGCAPIMRLAMWDAGTYVNTRTGANGSIRYEE 63
CC | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
CC 5 PTVSSEDYKKAKEKRRKRLGLIAEKNCAPILRLAMHSAGTDCQSRGCGPGTIRKQAE 64

QY 64 YTHGSNAKGLAIDLLERIKAKHRTIADLHQLAGVAVVEYTGPPYETIPGRDSSVC 123
D 65 LAHGANNMIDIAVRLIEIKIQPPLVSYADYQLAGVAVVEITGGPEVFPFRGREDKPEP 124
QY 124 PREGRLPAKGAFLHRIEYR-MGLTQKDIVALSGSHSLGAKPERSGFGAWTRDPLK 182
D 125 PREGRLPATATGSDHRLRVFKAMGLSDQDIVALSGHITCAHAKENSGFEGPMTSNPLI 184
QY 183 FDNSEYFELLKGESEGLKLPDTRALDDPFRRYVELYAKDEDEVFKDAVESHKRLSEL 242
D 185 FDNSEYFELLKGEKDGLLQLPSDKALLDYSFRPLVEKYADEDEVFADVAHLKLSL 244
QY 243 GF 244
D 245 GF 246

RESULT 3
CCPR_YEAST STANDARD; PRT; 361 AA.
ID CCPR_YEAST P00431;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cytochrome c peroxidase, mitochondrial precursor (EC 1.11.1.5) (CCP).
GN CCP1 OR CCP OR CPO OR YKR066C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetia; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BY939;
RA Platoni M., Miyazaki W., Jayaraman K., Kaput J.;
RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA van Vliet-Reedijk J.C., Planta R.J.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=83082819; PubMed=6294090;
RA Kaput J., Goltz S., Blobel G.;
RT "Nucleotide sequence of the yeast nuclear gene for cytochrome c
peroxidase precursor. Functional implications of the pre sequence for
protein transport into mitochondria.";
RL J. Biol. Chem. 257:115054-15058 (1982).
RN [4]
RP SEQUENCE OF 68-361.
RA MEDLINE=81108305; PubMed=6257176;
RA Takio K., Tiliak K., Ericsson L.H., Yonetani T.;
RT "Primary structure of yeast cytochrome c peroxidase. II. The complete
amino acid sequence.";
RL Arch. Biochem. Biophys. 203:615-629 (1980).
RN [5]
RP SEQUENCE OF 253-332 FROM N.A.
RC MEDLINE=82265845; PubMed=6286684;
RA Goltz S., Kaput J., Blobel G.;
RT "Isolation of the yeast nuclear gene encoding the mitochondrial
protein, cytochrome c peroxidase.";
RL J. Biol. Chem. 257:11186-11190 (1982).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RC MEDLINE=85030410; PubMed=6092361;
RA Finzel B.C., Poulos T.L., Kraut J.;
RT "Crystal structure of yeast cytochrome c peroxidase refined at 1.7-A
resolution.";
RL J. Biol. Chem. 259:13027-13036 (1984).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANTS.
RC MEDLINE=91002554; PubMed=2169873;

RA Wang J.M., Mauro M., Edwards S.L., Oatley S.J., Fishel L.A.,
RA Asiford V.A., Xiong N.-H., Kraut J.;
RT "X-ray structures of recombinant yeast cytochrome c peroxidase and
three heme-cleft mutants prepared by site-directed mutagenesis.";
RL Biochemistry 29:7160-7173 (1990).
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -1- CATALYTIC ACTIVITY: 2 ferrocyclochrome c + H(2)O(2) = 2
CC ferrocyclochrome c + 2 H(2)O.
CC -1- SUBUNIT: FORMS A ONE-TO-ONE COMPLEX WITH CYTOCHROME C.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. CYTOCHROME C
CC PEROXIDASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J62422; CAA44288.1; -;
DR EMBL: X01468; AAA88709.1; -;
DR EMBL: J01321; AAA88710.1; -;
DR EMBL: Z28291; CAA82145.1; -;
DR PIR: S19064; OPHYC.
DR PDB: 2CYP; 15-APR-93.
DR PDB: 1CCP; 15-OCT-94.
DR PDB: 2CCP; 15-APR-93.
DR PDB: 3CCP; 15-APR-93.
DR PDB: 4CCP; 15-APR-93.
DR PDB: 5CCP; 31-OCT-93.
DR PDB: 6CCP; 31-OCT-93.
DR PDB: 7CCP; 31-OCT-93.
DR PDB: 2PCP; 15-JUL-93.
DR PDB: 2PCG; 15-JUL-93.
DR PDB: 1CCB; 31-OCT-93.
DR PDB: 1CCG; 31-OCT-93.
DR PDB: 1CCE; 31-JUL-94.
DR PDB: 1CCG; 31-JUL-94.
DR PDB: 1CCT; 07-JUL-97.
DR PDB: 1CCJ; 23-JUL-97.
DR PDB: 1CCK; 13-JAN-99.
DR PDB: 1CCL; 13-JAN-99.
DR PDB: 1CMP; 31-JAN-94.
DR PDB: 1CMT; 31-JAN-94.
DR PDB: 1CMT; 10-JUL-95.
DR PDB: 1CMT; 10-JUL-95.
DR PDB: 1DCC; 31-JUL-94.
DR PDB: 2CEP; 31-AUG-94.
DR PDB: 1CEP; 01-NOV-94.
DR PDB: 1CPE; 01-NOV-94.
DR PDB: 1CPG; 01-NOV-94.
DR PDB: 1A2F; 13-JAN-99.
DR PDB: 1A2G; 13-JAN-99.
DR PDB: 1A4A; 23-JUL-97.
DR PDB: 1AC4; 04-SEP-97.
DR PDB: 1AC8; 04-SEP-97.
DR PDB: 1AEB; 04-SEP-97.
DR PDB: 1AEB; 04-SEP-97.
DR PDB: 1AEE; 04-SEP-97.
DR PDB: 1AEE; 04-SEP-97.
DR PDB: 1AEG; 04-SEP-97.
DR PDB: 1AEG; 04-SEP-97.
DR PDB: 1AEG; 04-SEP-97.
DR PDB: 1AEM; 04-SEP-97.
DR PDB: 1AEM; 04-SEP-97.
DR PDB: 1AEN; 04-SEP-97.
DR PDB: 1AEO; 04-SEP-97.
DR PDB: 1AEO; 04-SEP-97.

DR	PDB: 1AES: 04-SEP-97.	
DR	PDB: 1AET: 04-SEP-97.	
DR	PDB: 1AEU: 04-SEP-97.	
DR	PDB: 1AEV: 04-SEP-97.	
DR	PDB: 1ATC: 08-NOV-96.	
DR	PDB: 1CFY: 07-DEC-95.	
DR	PDB: 3CCX: 10-JUL-95.	
DR	PDB: 4CCX: 10-JUL-95.	
DR	PDB: 1BVA: 23-SEP-98.	
DR	PDB: 1BEJ: 21-OCT-98.	
DR	PDB: 1BEK: 21-OCT-98.	
DR	PDB: 1BEM: 21-OCT-98.	
DR	PDB: 1BEP: 21-OCT-98.	
DR	PDB: 1BEQ: 21-OCT-98.	
DR	PDB: 1BES: 21-OCT-98.	
DR	PDB: 1B19: 13-JAN-99.	
DR	SGD: S0001774; CCPL.	
DR	InterPro: IPR002016; Peroxidase.	
DR	Pfam: PF00141; peroxidase; 1.	
DR	PRINTS: PR00458; PEROXIDASE.	
DR	PROSITE: PS00435; PEROXIDASE_1; 1.	
DR	PROSITE: PS00436; PEROXIDASE_2; 1.	
KM	Oxidoreductase; Peroxidase; Heme; 3d-structure; Mitochondrion; Transil peptide; Polymorphism.	
KM	Transil peptide; Polymorphism.	
FT	TRANSIP	1
FT	CHAM1	67
FT	ACT_SITE	68 361
FT	ACT_SITE	115 115
FT	ACT_SITE	119 119
FT	ACT_SITE	242 242
FT	VARIANT	33 33
FT	VARIANT	120 120
FT	VARIANT	219 219
FT	MUTAGEN	258 258
FT	CONFLICT	41 41
FT	CONFLICT	62 62
FT	CONFLICT	145 146
FT	CONFLICT	231 231
FT	STRAND	74 74
FT	TURN	79 80
FT	HELIX	83 99
FT	TURN	100 102
FT	HELIX	103 106
FT	TURN	107 107
FT	HELIX	110 121
FT	TURN	122 123
FT	STRAND	125 125
FT	TURN	126 129
FT	STRAND	130 130
FT	TURN	134 135
FT	HELIX	137 139
FT	HELIX	141 144
FT	TURN	145 145
FT	HELIX	147 149
FT	TURN	150 152
FT	HELIX	153 165
FT	TURN	167 168
FT	HELIX	171 185
FT	TURN	186 187
FT	STRAND	193 193
FT	HELIX	202 204
FT	HELIX	218 226
FT	TURN	227 229
FT	HELIX	232 243
FT	STRAND	246 247
FT	HELIX	249 252
FT	STRAND	256 257
FT	TURN	262 263
FT	HELIX	268 275
FT	STRAND	278 282
FT	TURN	284 285
FT	STRAND	288 292
FT	TURN	293 294
FT	STRAND	297 298

```

FT      HELIX      300      307

Query Match          30.5%; Score 457; DB 1; Length 361;
Best Local Similarity 38.4%; Pred. No. 1.le-31;
Matches 93; Conservative 46; Mismatches 85; Indels 18; Gaps 3;

OY      29 GCAPIMRLAMHWAGCYDVNTRTGA--NSISIVEEYRHGNSAGLKIAIDLLEPIKAKHP 87
      | : ::::: ||| : | : | : : : : : | : : : : | : : : | : : : |
DB      108 GYGVPLVRLAMHNSGTMKDHDNTGSGYGGTYRKKKEFPDPSNAGQNGFKLEPIKEFP 167
OY      88 KITTYADHOLAGVAAVEVTGPTVEITPERBRS--SVCPREGRLPDAAKKAAPHLDIFYR 145
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      168 MISGGDLFSLGCVTAAGEMGPKIIPRCGRVTPEDDTTPDNGRLPDADKADADYKRTFFQR 227
OY      146 MGLTKDKIVALSGSHLKGAPHPERSGFDGAWTRDPIKFDNSYFLLKGE----- 195
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      228 LNMNDREVVALMGHAHGKTHLKNSGYEGPGCAANNVETNEFYINLNMEDKLEKNDANN 287
OY      196 -----SEGLKLPIPRDALDDPEFRKYVELYAKDEYFFPKYASHKLSLGLGTPSSG 250
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      288 EQWDSKSGYMWLPDYSLLQDPKYLSTVEKYANDQDKFFKFSKAFKLELNGTTPPKDA 347
OY      251 PA 252
      | :
DB      348 PS 349

RESULT 4
CATA_BACST
ID      CATA_BACST      STANDARD;      PRT;      735 AA.

AC      P14412;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
EN      PEA OR CAT.
OS      Bacillus stearothermophilus.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group;
OC      Bacillus/Staphylococcus group; Geobacillus.
OX      NCBI_TaxID:1422;
RN      [1]
RP      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC      SPRAIN-ATCC 8005 / IAM11001;
RX      MEDLINE-89359121; PubMed-2670897;
RA      Loperasert S., Negro S., Okada H.;
RT      "Cloning, nucleotide sequence, and expression in Escherichia coli of the Bacillus stearothermophilus peroxidase gene (peaA).";
RL      J. Bacteriol. 171:4871-4875(1989).
RN      [2]
RP      REVISIONS.
RA      Trakulnaleamsai S., Alhara S., Miyai K., Suga Y., Yomo T., Negro S.,
RA      Urahe I.;
RL      Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE-99116998; PubMed-9920270;
RA      Matsura T., Miyai K., Trakulnaleamsai S., Yomo T., Shima Y.,
RA      Miki S., Yamamoto K., Urahe I.;
RT      "Evolutionary molecular engineering by random elongation
RT      mutagenesis.";
RL      Nat. Biotechnol. 17:58-61(1998).
CC      -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC      BROAD-SPECTRUM PEROXIDASE ACTIVITIES.
CC      -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
CC      -1- COFACTOR: TWO PROTOHEME IX GROUPS.
CC      -1- SUBUNIT: HOMODIMER.
CC      -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC      PEROXIDASE/CATALASE SUBFAMILY.
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CC EMBL; M29876; AAA22655.1; -
DR EMBL; AB020234; BAA37114.1; -
DR PIR; J50520; J50520.
DR HSSP; P00431; ICCK.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase.1.
DR PRINTS; PRO0458; PEROXIDASE.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS00436; PEROXIDASE_2; 1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
FT ACT_SITE 97 97
FT BINDING 101 101 BY SIMILARITY.
FT SEQUENCE 735 AA; 82989 MW; 7131204A8BFAEF1 CRC64;
SO

Query Match 21.2%; Score 317; DB 1; Length 735;
Best Local Similarity 29.4%; Pred. No. 2.6e-19;
Matches 100; Conservative 39; Mismatches 85; Indels 116; Gaps 11;

QY 32 PIMRLAHMDGTYDVTNRTGAGN-GSIRYEBEYTHGSGNAGIKTAIDLLEPIKAKH-PKI 89
D 93 PLFIRMAHMGATRYIRIGRGAGSTGTORFAPLNSWPNANLMDKARLLMLPKKYGKMKI 152
QY 90 TYADLHQLAGVAVVETGGPTVEFIPIGRD----- 119
D 153 SWADLFIILGNVAIESMGCKITIGGCGVADVWHPEEDYVWSEKMWLASERYSGDRELEEN 212
QY 120 -----SSVCPR--BGRLPDANKGAPHLRDIIFYRMGLTDKIDVAL-SGSHSLGKAH- 166
D 213 PLAAVOMGLIYVNEPGPGPK-PDPKAARADIREFRMRGMNDEEVALIAGHTFGKAHG 271
QY 167 -----PE-----RSGFGCAWTRDPLKEDNSYFLELL 192
D 272 AGPATNVPPEEPAEPIEAQGLGMISSYGKSGKSDTITSGIGAWMPPTQMDTSYF-DML 330
QY 193 KGESEGLKLP-----TDKALLDDEFRFRVYE 219
D 331 FGYDMWLTRSPAGAMQMAVVPDEKDLAPDAEDBSKVPYMMMTTDLALRDPREYETIAR 390
QY 220 LYAKDEVFPRDYAESHKLS--ELGFTPRSSGPASTRSD 257
D 391 RFHNPFEFAFAFAWFKLTHRDWGPRTYRLGPEVPKED 430

RESULT 5
CATA_YERPE STANDARD; PRT; 737 AA.
ID CATA_YERPE
AC 09X6B0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase) (Antigen 5).
GN KATY OR YPO3319.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OC NCBI_TaxID=632;
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-KIM;
RX MEDLINE=99255535; PubMed=10322012;
RA Garcia E., Nedialkov Y.A., Elliott J., Motin V.L., Brubaker R.R.;
RT "Molecular characterization of Kaly (antigen 5), a thermoregulated
chromosomally encoded catalase-peroxidase of Yersinia pestis.";
RL J. Bacteriol. 181:3114-3122(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;

RA Parkhill J., Wren B.W., Thomson N.R., Tiltall R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Terraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagels K., Kalyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) -> OXIDIZED DONOR + 2 H(2)O.
CC -1- COFACTOR: TWO PROTHEME IX GROUPS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).

CC EMBL; AF135170; AAD37313.1; -
DR EMBL; AJ414156; CAC92551.1; -
DR HSSP; P00431; 1B29.
DR InterPro: IPR002016; Peroxidase.
DR Pfam; PF00141; peroxidase.1.
DR PRINTS; PRO0458; PEROXIDASE.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS00436; PEROXIDASE_2; 1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
FT ACT_SITE 99 99 BY SIMILARITY.
FT ACT_SITE 103 103 BY SIMILARITY.
FT BINDING 264 264 PROXIMAL HEME LIGAND (BY SIMILARITY).
FT SEQUENCE 737 AA; 81365 MW; DB870BC41ABD469A CRC64;
SO

Query Match 19.6%; Score 294; DB 1; Length 737;
Best Local Similarity 28.3%; Pred. No. 2.4e-17;
Matches 93; Conservative 33; Mismatches 91; Indels 112; Gaps 9;

QY 32 PIMRLAHMDGTYDVTNRTGAGN-GSIRYEBEYTHGSGNAGIKTAIDLLEPIKAKH-PKI 89
D 95 PFIIRMAHMGATRYIRIGRGAGGQGRFEPILNSWPNANLMDKARLLMLPKKYGKMKI 154
QY 90 TYADLHQLAGVAVVETGGPTVEFIPIGRD-----SSVCPREGRL----- 129
D 155 SWGDLMLVLTGNVALESMSGFKTLGFAGGREDWQSDLYWYAGANKMLSPNRKNGKLPRL 214
QY 130 -----PDAKKGAPHLRDIIFYRMGLTDKIDVAL-SGSHSLGKAH----- 166
D 215 AATOMGLIYVNEPGNGKPDVPAAKKDIREAFARMAAMDEETVALIAGHTFGKAHGAAS 274
QY 167 PER-----SGFDGAWTRDPLKEDNSYFLELLKG 194
D 275 PEKICGAAPGAGLEQGLGANKCGSGNKDITISGLEGAWTIDPFTFTQYLSNLYKH 334
QY 195 E-----SEGILKLPDKALLDDEFRFRVYELAKD 224
D 335 EFWLTKSPAGAMQMKPKNAANVPDADPTKFNHPLMPTTDLALKVDEYKKTITTRFLEN 394
QY 225 EDVFEKDYAESHKLSLSEGTTPRSSGPAS 253
D 395 PEERMAAFARAFKLT-----THRDGPRPA 418

RESULT 6
CATA_HALMA STANDARD; PRT; 731 AA.
ID CATA_HALMA
AC 059651;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
GN PERA.
OS Halosarcina marismortui (Halobacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Halosarcina.
OX NCBI_TaxID=2238;
RN [1]
RP SEQUENCE FROM N.A.
RA Franzetti B., Cannac-Caffrey V., Petillot Y., Hudry-Clergeon G.,
RA Gagnon J., Zaccal G.;
RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) -> OXIDIZED DONOR + 2 H(2)O.
CC -1- COFACTOR: TWO PROTHEME IX GROUPS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
CC -----
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CC -----
DR EMBL; Y16851; CAAT6423.1; -.
DR HSSP; P00431; ICCK.
DR InterPro; IPR002016; Peroxidase.
DR Pfam; PF00141; peroxidase; 1.
DR PRINTS; PR00458; PEROXIDASE.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS00436; PEROXIDASE_2; 1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
FT ACT_SITE 92 92
FT ACT_SITE 96 96
FT BINDING 259 259 BY SIMILARITY.
FT BINDING 259 259 PROXIMAL HEME LIGAND (BY SIMILARITY).
SQ SEQUENCE 731 AA; 81383 MW; 0E12DF0CF72FF3A3 CRC64;
Query Match 18.7%; Score 280.5; DB 1; Length 731;
Best Local Similarity 27.5%; Pred. No. 3.4e-16;
Matches 92; Conservative 39; Mismatches 88; Indels 115; Gaps 11;
DY 32 PIMRLAMHNDGTY-DVNTFRGGANGSTRYEETVHGSNAKLTALDLEPIKAKH-PKI 89
DY 88 PLFIRMAHNSAGTYRTADRGGAAGRGQRFAPINSMPPNANLNDKARLLLPKORYGOKI 147
DY 90 TYADLHOLAGVVAEVTGPTVEEIPGRDSSVCPRE-----GR 128
DY 148 SWADLMILAGVVAEVTGPTVEEIPGRDSSVCPRE-----GR 128
DY 148 SWADLMILAGVVAEVTGPTVEEIPGRDSSVCPRE-----GR 128
DY 121 -----SVCPR--EGRLPDANKGAPHLIDYFMGLTDKIDVAL-SCGSHSGKAH- 166
DY 208 GLGASVYGLIYVNEGPGDN-PDPEASAKNIRQTFRAMNDKEVALIAGHTGKVAG 266
DY 167 ---PER-----SGFGAATRDPLKDNSTFLEL 191
DY 267 ADDEENLGPPEAPLIEQGLGWMKNKNGSKGEMITSGIEGPTOSTPEMDKYINNL 326
DY 192 L-----KG-----ESEGLKLPDKLLDPEFRRYVE 219
DY 327 LDYTWBEPKGGGAGMOMAPKSEELKNSVPDAHDPEKOTPMMLTTDLALKRPDYREVME 386
DY 220 LYAKDEDFVFKDYAESHKLS--ELGFTPRSSGP 251
DY 387 TFOENPMEFGMNAKAWYKLTFRDGRPPERFLGP 420
RESULT 7
CATA_HALN1 STANDARD; PRT; 720 AA.
AC 073955; Q9HHP5;

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase)
GN PERA OR VNC6294G.
OS Halobacterium sp. (strain NRC-1), and
OS Halobacterium salinarum.
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091, 2242;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1; PLASMID=PNRC200;
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahlras G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorson V., Sirogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo T.A.,
RA Leitner B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlshroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.,
RA "Genome sequence of Halobacterium species NRC-1";
RA Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=H. salinarum;
RA Salin M.L., Long S.;
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) -> OXIDIZED DONOR + 2 H(2)O.
CC -1- COFACTOR: TWO PROTHEME IX GROUPS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
CC -----
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CC -----
DR EMBL; AE005159; AAC20931.1; -.
DR EMBL; AF069761; AAC23534.1; -.
DR HSSP; P00431; 1B39.
DR InterPro; IPR002016; Peroxidase.
DR Pfam; PF00141; peroxidase; 1.
DR PRINTS; PR00458; PEROXIDASE.
DR PROSITE; PS00435; PEROXIDASE_1; 1.
DR PROSITE; PS00436; PEROXIDASE_2; 1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; Plasmid;
KW Complete proteome.
FT ACT_SITE 79 79 BY SIMILARITY.
FT ACT_SITE 83 83 BY SIMILARITY.
FT BINDING 248 248 PROXIMAL HEME LIGAND (BY SIMILARITY).
SQ SEQUENCE 720 AA; 80476 MW; FB88823BCD3CB2E9 CRC64;
Query Match 18.5%; Score 276.5; DB 1; Length 720;
Best Local Similarity 27.1%; Pred. No. 7.3e-16;
Matches 91; Conservative 41; Mismatches 87; Indels 117; Gaps 11;
DY 32 PIMRLAMHNDGTY-DVNTFRGGANGSTRYEETVHGSNAKLTALDLEPIKAKH-PKI 89
DY 75 PLFIRMAHNSAGTYRTADRGGAAGRGQRLPPVDSWPDNVLAKARLLLPKORYGOKI 134
DY 90 TYADLHOLAGVVAEVTGPTVEEIPGRDSSVCPRE-----GR 128
DY 135 SWGDLIILAGVVAEVTGPTVEEIPGRDSSVCPRE-----GR 128


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OY 129 L-----PDAKKGAPHLRDIYRNGLTDKDVAL--SGGSHLGKA 165
DB 194 LKRWPLNTWGLIYVNEPEGNGEPDLEGSAKNIRESGKAMANDKEFTVALIAGHGFGKY 253
OY 166 H-----PER-----SGFDGAMTRDPLKFDNSYFL 189
DB 254 HGDADPEENVGAPPAAPLEIKGGLGWNEFEGECKGPDPTTSGIEGPMWNTPTQWDMSTYVD 313
OY 190 ELL-----KG-----ESGKLTLPDKALLDDPEFRY 217
DB 314 NILEYEMPEKPGGAMQMTTKSGELNESAPGVQDPTDEDVMMLTVALKNDPPDYREV 373
OY 218 VELYANDVEDFFKDYAESHKKL--SELGTPRSSGP 251
DB 374 LETFOENPREFOQSFSAWKYKLIHRDMGSEFRLGP 409

RESULT 8
CATALLEGPN
ID CATA_LEGPN STANDARD; PRT; 749 AA.
AC 09MVB9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
GN KATG.
OS Legionella pneumophila.
OC Bacteria: Proteobacteria: gamma subdivision; Legionellaceae group;
OC Legionellaceae: Legionella.
OX NCBI_Taxid=446;
RN [1]
RP SEQUENCE FROM N.A.
RA Amemura-Maekawa J., Watanabe H.;
RA STRAIN=AA511;
RT "Legionella pneumophila catalase-peroxidase gene."
RL Submitted (SEP-1998) to the EMBL/Genbank/DDBJ databases.
CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
CC -1- COFACTOR: TWO PROTOHEME IX GROUPS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
CC -----
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CC -----
DB EMBL: AB017595; BAA78342.1; ...
DB HSSP: P00431; IRYC.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00414; Peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE; 1.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
KM Oxidoreductase: Peroxidase; Iron; Heme; Hydrogen peroxide.
FT ACT_SITE 104 104 BY SIMILARITY.
FT ACT_SITE 108 108 BY SIMILARITY.
FT BINDING 270 270 PROXIMAL HEME LIGAND (BY SIMILARITY).
SQ SEQUENCE 749 AA; 82914 MW; 19E7931C472973C8 CRC64;

Query Match 18.2% Score 272.5; DB 1; Length 749;
Best Local Similarity 27.3%; Pred. No. 1.7e-15;
Matches 89; Conservative 37; Mismatches 91; Indels 109; Gaps 9;
OY 32 PMLRLAMHDAGTYDVNTGGANGSI-RYEERYTHGSNAGKIALDLEPIAKH-PRI 89
DB 100 PLEIRMSWMAAGTYRIRYDGRGANGGQRFAPQNSPMDNANLDMKARLLMPKIKOKGKRI 159
OY 90 TYADLHQLAGVAVVEVTGGPTVEFTIPGRD-----SSVCPREGRL--- 129

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DB 160 SMADLLIVLGNVAMESGFEFTIGFAGGREDWAEAINIMGPEGKWEISKRODKGLERP 219
OY 130 -----PDAKKGAPHLRDIYRNGLTDKDVAL--SGGSHLGKAH--- 166
DB 220 LAATWGLIYVNEPEGNGVDPPLAAAEKIRETGAMANDDEFTVALIAGHAGKTRGAA 279
OY 167 -----PE-----RSGFDGAMTRDPLKFDNSYFL--- 191
DB 280 SGKYLGPAPPAAGIEBQGGWKNYSYSGKGDITTSGLBEGAMVYTLTHMSHNTLQNLFN 339
OY 192 --LKGESEG-----LKLPTDKALLDDPEFRYELVA 222
DB 340 NMWKTSPPGALQWVPENSSMVPDAPDPSSKRHAPVMTLTLALFPVYSIAKRL 399
OY 223 KDDEVFEXDYAESHKKLSLGLTPRS 248
DB 400 DNEKFDAPARAWFKLIHRDMGPRS 425

RESULT 9
CATALLEGPN
ID CATALLEGPN STANDARD; PRT; 741 AA.
AC 028050;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
GN PERA OR AF2233.
OS Archaeoglobus fulgidus.
OC Archaea: Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_Taxid=2234;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RA MEDLINE=98049343; PubMed=9389475;
RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.R., Peterson J.D.,
RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodok A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton P.W., Spriggs T., Artlich P., Kalne B.P., Sykes S.M.,
RA Sadon P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
CC -1- COFACTOR: TWO PROTOHEME IX GROUPS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
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CC -----
DB EMBL: AE000951; AAB89022.1; ...
DB HSSP: P48534; IAPX.
DR TIGR: AF2233; ...
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00414; Peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.

```

DR PROSITE: PS00435; PEROXIDASE_1; 1.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
 FT Complete proteome.
 FT ACT_SITE 83 BY SIMILARITY.
 FT BINDING 87 BY SIMILARITY.
 FT BINDING 249 PROXIMAL HEME LIGAND (BY SIMILARITY).
 SO SEQUENCE 741 AA; 84854 MW; A931DF34F050FC63 CRC64;
 Query Match 17.7%; Score 265; DB 1; Length 741;
 Best Local Similarity 27.0%; Pred. No. 7.2e-15;
 Matches 99; Conservative 39; Mismatches 102; Indels 126; Gaps 14;
 QY 7 DAELYROY-----DRARRAFRLAIKAK-----GCAPIMRLAMHDGTYDVNRTG 52
 DB 40 DDIYEEVENDLIDAVIRDLKELMRSSQDMWPADEFGHYGLFRLMWSAGSYRIEDGRG 99
 QY 53 GA-NGSIRYEEETHTSGNAGLKAIDLEPIKAKH-PKITYADLHOLAGVAAVEVNG--- 107
 DB 100 GARDSIRPRPLNMDNINLDAIKRLNLPKIKKYGKRLSMADLIILAGTVAMEDMGVKL 159
 QY 108 -----GPRVEFIPIGRDSS-----VCPRI-EGRLPD 131
 DB 160 FCFALGREDIFEPDESPOGPEEEMLTAKRKEKELEPRPAATEMGLIYVNPBGCGNPD 219
 QY 132 AKKGAPHLADIFYRMGLTQKDIYAL-SGGHSLGKAH-----PE----- 168
 DB 220 PLGSAQELIVAFRRMGMDDEETVALLAGHAFCKGACGAPADYLGDPSSSPIEMOGLW 279
 QY 169 -----RSGFDGAWTRDPLKFPNSYF-----LELLK---GSEGLK--- 201
 DB 280 KYNYGKSGSDFTSGLEVTWSPTRPKGINVIRLIFTYEMLEKPKAPKNQVAADAP 339
 QY 202 -----LPTDKALLDDPEFRYVELYAKDEVEFKDYASHKRLSELGFT 245
 DB 340 IIPDAHDPKKHRRPMLTADIALRFPERSKIARFLNPEDEFEKAFALAWYKLT-----T 394
 QY 246 PRSSGP 251
 DB 395 HRDMGP 400
 RESULT 10
 CATA_ECOLI
 ID CATA_ECOLI STANDARD; PRT; 726 AA.
 AC P13029;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peroxidase/catalase HPI (EC 1.11.1.6) (Catalase-peroxidase)
 DE (Hydroperoxidase I).
 GN KATG OR B3942.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_Taxid=562;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=8831956; PubMed=3045098;
 RA Tliges-Raine B.L., Doble B.W., Mulvey M.R., Sorby P.A., Loewen P.C.;
 RT "Nucleotide sequence of katg, encoding catalase HPI of Escherichia
 RT coli.";
 RL J. Bacteriol. 170:4415-4419(1988).
 RN [2]
 RP SEQUENCE OF 1-339 FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=93347969; PubMed=8346018;
 RA Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
 RT "Analysis of the Escherichia coli genome. III. DNA sequence of the
 RT region from 87.2 to 89.2 minutes.";
 RL Nucleic Acids Res. 21:3391-3398(1993).
 RN [3]
 RP SEQUENCE OF 309-726 FROM N.A.
 RC STRAIN-K12 / MG1655;

RX MEDLINE=94089392; PubMed=8265357;
 RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
 RA Daniels D.L.;
 RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
 RT region from 89.2 to 92.8 minutes.";
 RL Nucleic Acids Res. 21:5408-5417(1993).
 CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
 CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES.
 CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
 CC -1- COFACTOR: TWO PROTOHEME IX GROUPS PER Tetramer.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- INDUCTION: BY HYDROGEN PEROXIDE.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
 CC PEROXIDASE/CATALASE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 HEME REGULATORY MOTIF (HRM).
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 CC
 DR EMBL; M21516; AAA24040.1; -;
 DR EMBL; L19201; AAB03074.1; -;
 DR EMBL; U00006; AAC43048.1; -;
 DR EMBL; AE000468; AAC76924.1; -;
 DR PIR; J50140; CSECHP.
 DR PIR; S40885; S40885.
 DR HSSP; P48534; IAPX.
 DR SWISS-2DPAGE; P13029; COLI.
 DR Ecogene; EG10511; katg.
 DR InterPro; IPR002016; Peroxidase.
 DR Pfam; PR00141; peroxidase; 1.
 DR PRINTS; PR00458; PEROXIDASE.
 DR PROSITE; PS00435; PEROXIDASE_1; 1.
 DR PROSITE; PS00436; PEROXIDASE_2; 1.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
 KW Complete proteome.
 KW ACT_SITE 102 BY SIMILARITY.
 FT ACT_SITE 106 106 BY SIMILARITY.
 FT BINDING 267 267 PROXIMAL HEME LIGAND (BY SIMILARITY).
 FT DOMAIN 15 20 HRM 1 (POTENTIAL).
 FT CONFLICT 621 621 A -> G (IN REF. 1).
 SO SEQUENCE 726 AA; 80023 MW; 24D32EBD5DE9BD6 CRC64;
 Query Match 17.2%; Score 257; DB 1; Length 726;
 Best Local Similarity 27.1%; Pred. No. 3.4e-14;
 Matches 91; Conservative 34; Mismatches 103; Indels 108; Gaps 10;
 QY 31 APTMLRLAMHDGTY-DVNTPTGANGSIRYEEETHTSGNAGLKAIDLEPIKAKH-PK 88
 DB 97 AGLEITMAHAGGTYRSIDRGAGRGQRFAPLNSWPDNVSIDKARLLMPTRKQGRK 156
 QY 89 ITYADLHOLAGVAAVEVNGPTVEFIPIGRD-----SSVCPREGRLPPAKKAGP 137
 DB 157 ISMADLFILAGVVALVLENSFFRGAGREDVWEPDLDVNNMGDEKAWLTHHPALAKAP 216
 QY 138 -----HLRDIIFYMGLTQKDIYAL-SGGHSLGKAH--- 166
 DB 217 LGATEMGLIYVNPBGPDHSGEPLSAAMAIIRATFGNMGNDEETVALLAGHRTLKTCGAG 276
 QY 167 -----PE-----RSGFDGAWTRDPLKFPNSYFLELLKG 194
 DB 277 PLSNWPDPPEAAPTEEOGLGNASTYSGVGADAITSGLEVWVOTPTQWSYFENLFKY 336
 QY 195 E-----SEGLK-----LPTDKALLDDPEFRYVELYAKD 224
 DB 337 EWWQTRSPAGATQFAVADAPETIIPDPDPSSKKRKTMTLVTLTRFDEFEKISRRLND 396
 QY 225 EDVFFKDYAESHKRLSELGFTPRSS--GPASTKSDV 258

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 CC -----
 DR EMBL: X83277; CAAS8266.1; .
 DR HSSP: P00431; ICCA.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF00141; Peroxidase; 1.
 DR PRINTS: PR00458; PEROXIDASE.
 DR PROSITE: PS00435; PEROXIDASE_1; 1.
 DR PROSITE: PS00436; PEROXIDASE_2; 1.
 KM Oxidoreductase: Peroxidase; Iron; Heme; Hydrogen peroxide.
 FT ACT_SITE 104 104 BY SIMILARITY.
 FT BINDING 270 270 PROXIMAL HEME LIGAND (BY SIMILARITY).
 SQ SEQUENCE 740 AA; 80575 MW; 8231FOF35397908 CRC64;
 Query March 17.0%; Score 254; DB 1; Length 740;
 Best Local Similarity 25.6%; Pred. No. 6.3e-14;
 Matches 99; Conservative 37; Mismatches 113; Indels 136; Gaps 12;
 32 PIMRLAHWDAGTYDYNRTGAGNSI-RYEETHTGSHNAGLKIADLLEPIKAKH-PRI 89
 100 PLFIRMAMHAGTYRIHNGRGAGGGMQRFAPLNSWPDASLDKARRLLMPKPKKTKGRL 159
 90 TYADLHQAAGVAVVVGCPYVEFLPGRD-----SSVCDESR 128
 160 SWADLIYAGNCALSMSEKTFEGFGVQWEPDEVYWGKEATWLGDERYSGKRDLENP 219
 129 L-----PDAKKGAP-----HLRDIYRMGLTDXDIALV-SGSHSIGKAH--- 166
 220 LAAYOMGLIYVNPAPNGNPDMAAVDIRFRRMAANDVTALIVGSHFGKTHGAG 279
 167 -----PE-----RSGFDGANTRDPLKEDNSYFLELLNG 194
 280 PADVGPPEAPAPLEBMGLGKMSYGTGTGKDAITSIEVVTNPTKMDNS-FLEITLG 338
 195 ESEGLKLP-----TDKALLDPPERRYVELTA 222
 339 YEWELTKSPAGAMQYTAGAGAGTIPPFPGSGSPMTLADLSLVDPIYETRRWL 398
 223 KDEVFEDYAESHKLL-SELGFTPRSSGP-----AST 254
 399 EHPELADFEPAKAWKYLHRDMGPVARYLGPLVPRQTLMDPVRVAVSHDLYGEAELASL 458
 255 KSDVSTAVVLAQSAVGAVAVAATVAG 281
 459 KSQILASGLIVSQLVSTAMAAASFRG 485
 RESULT 13
 CATA_MYCTU STANDARD; PRT; 740 AA.
 AC 008129; 057274; 057215; 008221; 050544; 050546; 050551; 050552;
 AC 050553; 050554; 050555;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peroxidase/catalase T (EC 1.11.1.6) (catalase-peroxidase T).
 GN KATG OR RV1908C OR MT1959 OR MTCY180.10.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN NCBI_TaxID-1773;
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN-H37RV;
 RX MEDLINE-93308108; PubMed-8320241;

RA Heyn B., Zhang Y., Poulet S., Young D., Cole S.T.;
 RT "Characterization of the katG gene encoding a catalase-peroxidase
 RT required for the isoniazid susceptibility of Mycobacterium
 RT tuberculosis";
 RT J. Bacteriol. 175:4255-4259(1993).
 RN [2]
 RP REVISIONS.
 RC STRAIN-H37RV;
 RA Cole S.T.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 25618;
 RA Cockerill F.R., Uhl J.R., Temesgen Z., Zhang Y., Stockman L.,
 RA Roberts G.D., Williams D.L., Kline B.C.;
 RT "Rapid identification of a point mutation of the Mycobacterium
 RT tuberculosis catalase-peroxidase (katG) gene associated with
 RT isoniazid resistance";
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-INH-RESISTANT STRAINS;
 RA Martilla H.J., Solin H., Huovinen P., Villanen M.K.;
 RT "katG gene mutations in isoniazid-resistant Mycobacterium
 RT tuberculosis strains isolated from Finnish patients";
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE-98295987; PubMed-9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence";
 RL Nature 393:537-544(1996).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP PARTIAL SEQUENCE FROM N.A., AND ISONIAZID RESISTANCE.
 RC STRAIN-H37RV;
 RX MEDLINE-92365822; PubMed-1501713;
 RA Zhang Y., Heyn B., Allen B., Young D., Cole S.T.;
 RT "The catalase-peroxidase gene and isoniazid resistance of
 RT Mycobacterium tuberculosis";
 RL Nature 358:591-593(1992).
 RN [8]
 RP SEQUENCE OF 1-94 FROM N.A.
 RC STRAIN-H37RV;
 RA Song J., Dereic V.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
 RP BROAD-SPECTRUM PEROXIDASE ACTIVITIES. MAY PLAY A ROLE IN THE
 RP INTRACELLULAR SURVIVAL OF MYCOBACTERIA.
 CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) -> O(2) + 2 H(2)O.
 CC -1- COFACTOR: TWO PROTOHEME IX GROUPS PER TETRAMER.
 CC -1- SUBUNIT: HOMODIMER (PROBABLE).
 CC -1- MISCELLANEOUS: DELETIONS OR DEFECTS IN KATG GENE CAUSE ISONIAZID
 CC (INH) RESISTANCE.

```

CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb.ch).
CC -----
DR EMBL: X68081; CAA48213.1; -
DR EMBL: 006258; AAB04159.1; -
DR EMBL: 040593; AAA85167.1; -
DR EMBL: 040595; AAA85169.1; -
DR EMBL: 041305; AAA85171.1; -
DR EMBL: 041306; AAA85172.1; -
DR EMBL: 041307; AAA85173.1; -
DR EMBL: 041308; AAA85174.1; -
DR EMBL: 041309; AAA85175.1; -
DR EMBL: 041310; AAA85176.1; -
DR EMBL: 041311; AAA85177.1; -
DR EMBL: 041312; AAA85178.1; -
DR EMBL: 041313; AAA85179.1; -
DR EMBL: 041314; AAA85180.1; -
DR EMBL: 297193; CAB10056.1; -
DR EMBL: AE007051; AAK46231.1; -
DR EMBL: AF002194; AAB63371.1; -
DR PIR: A40662; A40662.
DR PIR: S34036; S34036.
DR HSSP: P00431; 2PCB.
DR TIGR: MT1959; -.
DR TubercuList: Rv1908c; -.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE_1; 1.
DR PROSITE: PS00435; PEROXIDASE_1; 1.
DR PROSITE: PS00436; PEROXIDASE_2; 1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
KW Complete proteome.
FT ACT_SITE 104 104 BY SIMILARITY.
FT ACT_SITE 108 108 BY SIMILARITY.
FT BINDING 270 270 PROXIMAL HEME LIGAND (BY SIMILARITY).
FT VARIANT 300 300 W -> G (IN INH-RESISTANT STRAIN
H0892/92).
FT VARIANT 315 315 S -> T (IN INH-RESISTANT STRAINS
H0181/94, H0452/92, H0948/92 AND
H0169/93).
FT VARIANT 463 463 R -> L (IN INH-RESISTANT STRAIN
H0169/93).
FT VARIANT 501 501 P -> A (IN INH-RESISTANT STRAIN
H0948/92).
FT VARIANT 525 525 O -> P (IN INH-RESISTANT STRAIN
H0251/90).
FT VARIANT 587 587 L -> P (IN INH-RESISTANT STRAIN
15726/89).
FT VARIANT 700 700 S -> P (IN INH-RESISTANT STRAIN
H0004/93).
FT CONFLICT 234 234 G -> A (IN REF. 1).
SQ SEQUENCE 740 AA; 80604 MW; B43C03B533CDD89 CR664;
Query Match 17.0%; Score 254; DB 1; Length 740;
Best Local Similarity 25.3%; Pred. No. 6,3e-14;
Matches 98; Conservative 36; Mismatches 115; Indels 138; Gaps 11;
QY 32 PIMLRTHMGADGTYDVNRTGANGSI-RYEERYTGSNAGLKIADLLEPIKAKH-PRI 89
DB 100 PLETRAMHAGTYRTHDRGGAGGGMORFAPLNPWNASLIDKARRLLMPVKKTKGKTL 159
QY 90 TYADLHQLAGVAVEYTGPFVEFIFGRRD-----SSVCPREGR 128
DB 160 SWADLIVFAGNCALESMGKRTGFGRGVDMPEDEVYNGKEATWLDGDERYSQKRLDNP 219

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QY 129 L-----PDAKKGAPHLRDLIFYRMGLTDKQDVAL-SCGSHIGRAH---- 166
DB 220 LAAYVGLIYVNEGPNBNDPMAAAYVDIREFFRRAMNDVETALIVGHTFGKTHGAG 279
QY 167 -----PE-----RSGFGANTRODLKNDNSYFLELLG 194
DB 280 PADLVGPEPEAPLEQMGIGWSSSYGTGKDAITGIEVWMTNPTKWDNS-FLEILG 338
QY 195 ESEGLKLP-----PDKALLDDPEFRYVELTA 222
DB 339 YEMELTKSPAGAMQYATKAGACAGTTPDPFGGRSPYMLADLSLRVPYIERITRRRL 398
QY 223 KQEDVEFKDYASBHKKL--SELGFTPRSSGP-----AST 254
DB 399 EHPEELADEFAKAWYKLIHRDMGPVARYLGPVKQTLLMOPVPVAVSHDLVGEAEIASL 458
QY 255 KSDYSTAVYLAQSAVGVAANAAYVING 281
DB 459 KSOIRASGLTVSQLVSTAWAAASSFRG 485

RESULT 14
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ID CATP_MYCSM STANDARD; PRT; 739 AA.
AC Q59557; 005763;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Peroxidase/catalase T (EC 1.11.1.6) (Catalase-peroxidase T).
GN KATG.
OS Mycobacterium smegmatis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 700084 / MC(2)155;
RX MEDLINE=97023930; PubMed=8870251;
RA Billman-Jacobe H., Sloan J., Coppel R.L.;
RT "Analysis of Isoniazid-resistant transposon mutants of Mycobacterium
RT smegmatis.";
RL FEMS Microbiol. Lett. 144:47-52(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MC(2)1216;
RA Engler O., Telenti A.;
RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES. MAY PLAY A ROLE IN THE
CC INTRACELLULAR SURVIVAL OF MYCOBACTERIA.
CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
CC -1- COFACTOR: TWO PROTOHEME IX GROUPS PER TETRAMER.
CC -1- SUBUNIT: HOMODIMER (PROBABLE).
CC -1- MISCELLANEOUS: DELETIONS OR DEFECTS IN KATG GENE CAUSE ISONIAZID
CC (INH) RESISTANCE.
CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
CC PEROXIDASE/CATALASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: X98718; CAA67268.1; -
DR EMBL: 046844; AAC45275.1; -
DR HSSP: P48534; IAPX.
DR InterPro: IPR002016; Peroxidase.
DR Pfam: PF00141; peroxidase; 1.
DR PRINTS: PR00458; PEROXIDASE_1; 1.
DR PROSITE: PS00435; PEROXIDASE_1; 1.

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DR PROSITE: PS00436; PEROXIDASE.2; 1.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
 FT ACT_SITE 110 110 BY SIMILARITY.
 FT BINDING 114 114 BY SIMILARITY.
 FT BINDING 277 277 PROXIMAL HEME LIGAND (BY SIMILARITY).
 FT CONFLICT 51 51 L -> M (IN REF. 2).
 FT CONFLICT 214 214 D -> RT (IN REF. 2).
 FT CONFLICT 374 374 PRTA -> AHEDG (IN REF. 2).
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 Best Local Similarity 26.2%; Pred. No. 3.3e-13;
 Matches 88; Conservative 37; Mismatches 98; Indels 113; Gaps 10;
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 QY 90 TYADLHQLAGVAVEVTG-----GPTVEFIPGRDSSVCPREG 127
 DB 166 SWADLIYVAGNVALIEDMGFTAGFARGREDRWEPEEDVYVPEQEWLDDKRYGERDLEN 225
 QY 128 RL-----PDAKKGAPHLRDIIFYRMGLTDKIDVAL-SGGHSLGKAH-- 166
 DB 226 PLAAVOMGLIYVNEPGRNGNPDQASADIRETFGRAMANDVETALIVGHTFGTKHGN 285
 QY 167 -----PE-----RSGFDGAWTRDPLKEDNSYFLELTK 193
 DB 286 GDASLVGPEAPLEVEGLGMHNPQGTGVKDAITSGLEVTWTHPTKMDNS-FLBILY 344
 QY 194 GSEGLTKLP-----IDKALLDPEFRYVELY 221
 DB 345 GDEWELTKSPAGANQMKPKDNGWANSVPLPTPRAKTHPSMLTSDLALRVDPIYEQITRRW 404
 QY 222 AKDEVFYFKDAESHKKL--SELGTPRSSGSPASTK 255
 DB 405 LDHPEELAEFAKAWFKLHRDMGPTRYLGPVEPK 440
 RESULT 15
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 AC 031066:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
 GN KATG OR CC3043.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 OX NCBI_TaxID=69394;
 RN [1]
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 RC STRAIN=ATCC 19089 / CB15;
 RA MEDLINE=21173698; PubMed=11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Pockock I., Nelson W.C., Newton A., Stephens C., Pladde N.D., Ely B.,
 RA Debony R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Kouri H., Shetty J., Berry K.,
 RA Usterback T., Tran K., Wolf A., Yamaliev J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 RN [2]
 RP SEQUENCE OF 1-494 FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RA MEDLINE=98012985; PubMed=9352936;
 RA Steinman H.M., Fareed F., Weinstein L.;
 RT "Catalase-peroxidase of Caulobacter crescentus: function and role in
 RT stationary-phase survival.";
 RL J. Bacteriol. 179:6831-6836(1997).

CC -1- FUNCTION: BIFUNCTIONAL, EXHIBITING BOTH A CATALASE AND
 CC BROAD-SPECTRUM PEROXIDASE ACTIVITIES.
 CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
 CC -1- COFACTOR: TWO PROHEME IX GROUPS (BY SIMILARITY).
 CC -1- INDICTION: TWO PROHEME IX GROUPS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. BACTERIAL
 CC PEROXIDASE/CATALASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: AE005967; AAC25005.1; -;
 CC EMBL: AF027168; AAC45850.1; -;
 CC HSSP: P00431; IRYC.
 DR TIGR: CC3043; -;
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PF00141; peroxidase.1.
 DR PROSITE: PS00435; PEROXIDASE.1; 1.
 DR PROSITE: PS00436; PEROXIDASE.2; 1.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
 KW Complete proteome.
 FT ACT_SITE 102 102 BY SIMILARITY.
 FT ACT_SITE 106 106 BY SIMILARITY.
 FT BINDING 268 268 PROXIMAL HEME LIGAND (BY SIMILARITY).
 SQ SEQUENCE 737 AA; 80165 MW; D900742D04E02E97 CRC64;

Query Match 16.3%; Score 244.5; DB 1; Length 737;
 Best Local Similarity 26.4%; Pred. No. 4e-13;
 Matches 89; Conservative 37; Mismatches 98; Indels 113; Gaps 11;

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 QY 91 YADLHQLAGVAVEVTGPTVEFIPGRDSSVCPRE----- 126
 DB 159 WADLIYVAGNVALIESMGFTFGFAGRADOME-PEELLYNGPESTWLDKRYGERELDSP 217
 QY 127 -----GRL-----PDAKKGAPHLRDIIFYRMGLTDKIDVAL-SGGHSLGKAH-- 167
 DB 218 LGAVOMGLIYVNEPGRNGNPDPLASARDIRETFGRAMANDVETALIVGHTFGTKHGN 277
 QY 168 -----ERSGFGA-----WTRDPLKEDNSYFLELTK 194
 DB 278 DASLVGPEPGAIEAGFGWASKHGTGKPDAITGGPEVIWTPPTPRNSHFFFNLFKY 337
 QY 195 ESEGLTKLP-----TDKALLDPEFRYVELYAK 223
 DB 338 EWE-LTQSPAGAKOMAKNAPADIPDAPDNKTHVPRMITSIDLALRFPDPAVKISRRPYE 396
 QY 224 DEDVFYFKDAESHKKLS--ELGTPRSSGSPASTKSDV 258
 DB 397 NPDQFADAFARAWFKLHRDMGPTRYLGPVKEEL 433

Search completed: October 23, 2002, 13:56:44
 Job time : 17 secs

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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:56:19 ; Search time 14 Seconds
(without alignments)
507,703 Million cell updates/sec

Title: US-09-870-501-1
Perfect score: 1498
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCrUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	484	32.3	122	1	US-08-266-451B-18 Sequence 18, Appl
2	484	32.3	122	2	US-08-748-725-18 Sequence 18, Appl
3	454	30.3	294	2	US-08-459-499-16 Sequence 16, Appl
4	451.5	30.1	293	2	US-08-313-185-52 Sequence 52, Appl
5	451.5	30.1	293	2	US-09-082-614A-52 Sequence 52, Appl
6	273.5	18.3	745	2	US-08-674-887A-8 Sequence 8, Appl
7	273.5	18.3	745	3	US-08-951-844-8 Sequence 8, Appl
8	272.5	18.2	753	2	US-08-674-887A-6 Sequence 6, Appl
9	272.5	18.2	753	3	US-08-951-844-6 Sequence 6, Appl
10	257	17.2	726	2	US-08-313-185-49 Sequence 49, Appl
11	257	17.2	726	2	US-08-459-499-13 Sequence 13, Appl
12	257	17.2	726	2	US-09-082-614A-49 Sequence 49, Appl
13	254	17.0	740	1	US-08-418-782-7 Sequence 7, Appl
14	254	17.0	740	1	US-08-418-782-21 Sequence 21, Appl
15	254	17.0	740	1	US-08-228-662-7 Sequence 7, Appl
16	254	17.0	740	2	US-08-852-219-7 Sequence 7, Appl
17	254	17.0	740	2	US-08-852-219-21 Sequence 21, Appl
18	247.5	16.5	729	2	US-08-313-185-50 Sequence 50, Appl
19	247.5	16.5	729	2	US-08-459-499-14 Sequence 14, Appl
20	247.5	16.5	729	3	US-09-082-614A-50 Sequence 50, Appl
21	233	15.6	735	2	US-08-313-185-48 Sequence 48, Appl
22	233	15.6	735	2	US-08-459-499-9 Sequence 9, Appl
23	233	15.6	735	2	US-08-459-499-12 Sequence 12, Appl
24	233	15.6	735	3	US-09-082-614A-48 Sequence 48, Appl
25	219.5	14.7	652	2	US-08-313-185-53 Sequence 53, Appl
26	219.5	14.7	652	2	US-08-459-499-11 Sequence 11, Appl
27	219.5	14.7	652	3	US-09-082-614A-53 Sequence 53, Appl

28	217	14.5	731	2	US-08-313-185-51 Sequence 51, Appl
29	217	14.5	731	2	US-08-459-499-15 Sequence 15, Appl
30	217	14.5	731	3	US-09-082-614A-51 Sequence 51, Appl
31	193.5	12.9	313	2	US-08-671-320-15 Sequence 15, Appl
32	193.5	12.9	313	2	US-08-868-577-15 Sequence 15, Appl
33	190.5	12.7	313	2	US-08-671-320-17 Sequence 17, Appl
34	190.5	12.7	313	2	US-08-868-577-17 Sequence 17, Appl
35	171	11.4	344	4	US-09-024-532-4 Sequence 4, Appl
36	171	11.4	345	1	US-07-792-259-12 Sequence 12, Appl
37	171	11.4	364	1	US-07-792-259-17 Sequence 17, Appl
38	170	11.3	343	2	US-08-624-545-11 Sequence 11, Appl
39	170	11.3	343	2	US-09-235-736-1 Sequence 1, Appl
40	170	11.3	363	1	US-08-458-023B-6 Sequence 6, Appl
41	170	11.3	435	2	US-08-331-515A-2 Sequence 2, Appl
42	170	11.3	435	4	US-09-168-406A-2 Sequence 2, Appl
43	156.5	10.4	349	1	US-08-190-029A-10 Sequence 10, Appl
44	156.5	10.4	349	2	US-08-462-695-10 Sequence 10, Appl
45	151	10.1	324	2	US-08-671-320-11 Sequence 11, Appl

ALIGNMENTS

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RESULT 1
US-08-266-451B-18
; Sequence 18, Application US/08266451B
; Patent No. 5623054
; GENERAL INFORMATION:
; APPLICANT: Zhang et al.
; TITLE OF INVENTION: CIRCITER AFT PROTEINS AND USES
; NUMBER OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,451B
; FILING DATE: 23-June-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/219001
; TELEPHONE: (617) 542-8906
; TELEFAX: (617) 542-5070
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-266-451B-18

Query Match      32.3%; Score 484; DB 1; Length 122;
Best Local Similarity 75.4%; Pred. No. 2.6e-45;
Matches 95; Conservative 9; Mismatches 18; Indels 4; Gaps 1;

QY 166 HPERSGFDCAWTRDPLKPFNSYLELKGESGLKLPDKALDDPEFRRLVETLAKDE 225
DB 1 HPERSGFDCPMTQEPKPFNSYFVELKGESGLKLPDKLTLEDPEFRRLVETLAKDE 60
QY 226 DVFFDYAESHRKLSLGLTPRSSGPASTKSDVSTAVVLAQSAVGVAANAAYIAGIYAE 285
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DB 61 DAFEDYASHKSLSELGENPNSSAGKA-----VADSTILAQSAFGVAVAAGFYFE 116
QY 286 ASKRSK 291
DB 117 IKRKMK 122

RESULT 2

US-08-748-725-18
; Sequence 18, Application US/08748725
; Patent No. 5859346

GENERAL INFORMATION:

APPLICANT: Zhang et al.
TITLE OF INVENTION: CROCIER APT PROTEINS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,725
FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/266,451
FILING DATE: 23-June-1994
ATTORNEY/AGENT INFORMATION:

NAME: Lech, Karen F.

REGISTRATION NUMBER: 35,238

REFERENCE/DOCKET NUMBER: 00786/219002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 122

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-748-725-18

Query Match

Best Local Similarity 32.3%; Score 484; DB 2; Length 122;
Best Local Similarity 75.4%; Pred. No. 2, 6e-45;

Matches 95; Conservative 9; Mismatches 18; Indels 4; Gaps 1;

QY 166 HPERSGFGAWTRDPLKFNDSYFLELLKGESEGLKLPDKALLDDPEFRRLVETAKDE 225
DB 1 HPERSGFGDPWTOEPLKFNDSYFLELLKGESEGLKLPDKTLLDPEFRRLVETAKDE 60
QY 226 DVEFDYAEASHKSLSELGTPRSSSGPASTKSDYSTAVLAQSAVGVAVAAGFYFE 285
DB 61 DAFEDYASHKSLSELGTPRSSSGPASTKSDYSTAVLAQSAVGVAVAAGFYFE 116
QY 286 ASKRSK 291
DB 117 IKRKMK 122

RESULT 3

US-08-459-499-16
; Sequence 16, Application US/08459499
; Patent No. 5871912

GENERAL INFORMATION:

APPLICANT: Heym, Beate

APPLICANT: Cole, Stewart T.

APPLICANT: Young, Douglas B.

APPLICANT: Zhang, Ying

TITLE OF INVENTION: Nucleic Acid Probes, Sequences, and Methods

TITLE OF INVENTION: for Detecting Mycobacterium Tuberculosis Resistant to Isonl

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finegan, Henderson, Farabow, Garrett &

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.3

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,499

FILING DATE: 02-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/875,940

FILING DATE: 30-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/929,206

FILING DATE: 27-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/029,655

FILING DATE: 11-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03495, 0110-03000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 294 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-459-499-16

Query Match

Best Local Similarity 30.3%; Score 454; DB 2; Length 294;
Best Local Similarity 38.4%; Pred. No. 2e-41;

Matches 93; Conservative 46; Mismatches 85; Indels 18; Gaps 3;

QY 29 GCAPIMRLAMHDAGTYVNTRTGA-NGSIRYEEYTHGSNAGKLAIDLLEPIKARHP 87
DB 41 GYGPVLVRLAMHSGTWKHDNTGSGYGTFRKKEFNDSNAGLONGFLEPIKARHP 100
QY 88 KITAYLHLQAGVAAVEGCGPTVERIPGRBS--SYCPREGRLEDDAKKAPHLRDIYR 145
DB 101 WISSGFLSFGTAAVOENQGPRIWRCGRVDTPEDTTPDNGRLDADKADGAYVTFEQR 160
QY 146 MGITLDIYALSGHSLGKAHPERSGFGDAMTRDPLKFNDSYFLELLKGE----- 195
DB 161 LNNNDREYVALMCAHAGLTHLKNSEBPGWCAANNVFTNEYTLWLDMDKLEKNDANN 220
QY 196 -----SEGILKLPDKALLDDPEFRRLVETAKDEVEFKDAESHKSLSELGTPRSSG 250
DB 221 EQWDSKSGYMMLPDYSLIQDPKYLSTYKEVANDQDKFKDSKAFKLENGITFEPDA 280
QY 251 PA 252
DB 281 PS 282

DB 401 RYENPDERADAFKAKMYKLTNRDGMCKYRYLGEPEVPOEDL 441

RESULT 8

US-08-674-887A-6
; Sequence 6, Application US/08674887A
; Patent No. 5939300
; GENERAL INFORMATION:
; APPLICANT: Robertson, Dan E.
; APPLICANT: Sanjay, Indrajit
; APPLICANT: Adhikari, Robert S.
; TITLE OF INVENTION: CATALASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,887A
; FILING DATE: 03-JUL-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09015/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 753 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-674-887A-6

Query Match

Best Local Similarity 18.2%; Score 272.5; DB 2; Length 753;
Best Local Similarity 27.0%; Pred. No. 6.4e-21;
Matches 93; Conservative 36; Mismatches 96; Indels 119; Gaps 10;

QY 33 IMRLAMHAGTYDV-NFTTGGANGSIRYEEYTHGSNAGLKAIDLEPIKAKH-PRIT 90
DB 120 LMRAMHAGTYRIRIDGGGGGTSORPAPLNSWPDNVLKARLRLPIKKTGNKIS 179
QY 91 YADLHQLAGVAVEVYTGPTVEIPGRD-----SSVCPREGRL----- 129
DB 180 WADLMILAGTAVYESWGLPAYGFSFGVDIWEPEKDIYWGDEKEMLAPDEHYGVNKP 239
QY 130 -----PDAKKGAFLRDIFRMLGTLTKDIYAL-SGGHSLCK 164
DB 240 TMENPLAAVOMGLIYVNPBGVNGHDPRLTAQOVLTFARMAMNDEKTAALTAGGHTVGN 299
QY 165 AH-----PE-----RSGFDGAWTRDPLKFDNSYFL 189
DB 300 CHGNGNASALADPKRASDVENOGGLGNGNPMOGKASNAVTSGIEGAWTINPTKFDGTF- 358
QY 190 ELLKGESEGLKLP-----TDKALIDDPFERR 216
DB 359 DLLFGYNMELKKSPPAGAHMMEPIDIKKENKPYDASDPSIRHNPIMTDADMAIKVNPTRYA 418
QY 217 YVELYAKDEDVFFKDYAESHKLS--ELGFTPRSSGPASTKSDV 258

DB 419 ICEKEMADEPFFKTYFAKAMFKLTHRDLPKRSRYIGPEVPAPD 462

RESULT 9

US-08-951-844-6
; Sequence 6, Application US/08951844
; Patent No. 6074860
; GENERAL INFORMATION:
; APPLICANT: Robertson et al.
; TITLE OF INVENTION: Catalases
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,844
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/674,887
; FILING DATE: July 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles J. Herron
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 331400-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 753 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: Polypeptide
; US-08-951-844-6

Query Match

Best Local Similarity 18.2%; Score 272.5; DB 3; Length 753;
Best Local Similarity 27.0%; Pred. No. 6.4e-21;
Matches 93; Conservative 36; Mismatches 96; Indels 119; Gaps 10;

QY 33 IMRLAMHAGTYDV-NFTTGGANGSIRYEEYTHGSNAGLKAIDLEPIKAKH-PRIT 90
DB 120 LMRAMHAGTYRIRIDGGGGGTSORPAPLNSWPDNVLKARLRLPIKKTGNKIS 179
QY 91 YADLHQLAGVAVEVYTGPTVEIPGRD-----SSVCPREGRL----- 129
DB 180 WADLMILAGTAVYESWGLPAYGFSFGVDIWEPEKDIYWGDEKEMLAPDEHYGVNKP 239
QY 130 -----PDAKKGAFLRDIFRMLGTLTKDIYAL-SGGHSLCK 164
DB 240 TMENPLAAVOMGLIYVNPBGVNGHDPRLTAQOVLTFARMAMNDEKTAALTAGGHTVGN 299
QY 165 AH-----PE-----RSGFDGAWTRDPLKFDNSYFL 189
DB 300 CHGNGNASALADPKRASDVENOGGLGNGNPMOGKASNAVTSGIEGAWTINPTKFDGTF- 358
QY 190 ELLKGESEGLKLP-----TDKALIDDPFERR 216
DB 359 DLLFGYNMELKKSPPAGAHMMEPIDIKKENKPYDASDPSIRHNPIMTDADMAIKVNPTRYA 418
QY 217 YVELYAKDEDVFFKDYAESHKLS--ELGFTPRSSGPASTKSDV 258

Db	419	ICEKMADEYFKKTFKAKAMFKLTHRDLPKRSRYIGPEVPAEDL	462
		RESULT 10	
		US-08-313-185-49	
		Sequence 49, Application US/08313185	
		Patent No. 5851763	
		GENERAL INFORMATION:	
		APPLICANT: Heym, Beate	
		APPLICANT: Cole, Stewart	
		APPLICANT: Young, Douglas	
		APPLICANT: Zhang, Ying	
		APPLICANT: Honore, Nadine	
		APPLICANT: Telenti, Amalio	
		APPLICANT: Bodmer, Thomas	
		TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance	
		TITLE OF INVENTION: In Mycobacterium Tuberculosis	
		NUMBER OF SEQUENCES: 66	
		CORRESPONDENCE ADDRESS:	
		ADDRESSEE: Finegan, Henderson, Farabow, Garrett &	
		ADDRESS: Dunner	
		STREET: 1300 I Street, N.W.	
		CITY: Washington	
		STATE: D.C.	
		COUNTRY: USA	
		ZIP: 20005-3315	
		COMPUTER READABLE FORM:	
		MEDIUM TYPE: Floppy disk	
		COMPUTER: IBM PC compatible	
		OPERATING SYSTEM: PC-DOS/MS-DOS	
		SOFTWARE: Patent In Release #1.0, Version #1.25	
		CURRENT APPLICATION DATA:	
		APPLICATION NUMBER: US/08/313,185	
		FILING DATE: 12-OCT-1994	
		CLASSIFICATION: 435	
		ATTORNEY/AGENT INFORMATION:	
		NAME: Meyers, Kenneth J.	
		REGISTRATION NUMBER: 25,146	
		REFERENCE/DOCKET NUMBER: 02356, 0068-00000	
		TELECOMMUNICATION INFORMATION:	
		TELEPHONE: (202) 408-4000	
		TELEFAX: (202) 408-4400	
		INFORMATION FOR SEQ ID NO: 49:	
		SEQUENCE CHARACTERISTICS:	
		LENGTH: 726 amino acids	
		TYPE: amino acid	
		STRANDEDNESS: single	
		TOPOLOGY: linear	
		MOLECULE TYPE: peptide	
		US-08-313-185-49	
		Query Match	17.2%; Score 257; DB 2; Length 726;
		Best Local Similarity	27.1%; Pred. NO. 3e-19;
		Matches	91; Conservative 34; Mismatches 103; Indels 108; Gaps 10.
QY	31	APIMLRLAMHDAQTV-DVNTFRGTGANGSIRYEETTHGSSNAGIKTAIDLEPIKAKH-BK	88
Db	97	AGLFIRMAMHGACITRSIDRGAGACGQRFAPLNSMPDNLSDKARRLIMPIKQYCGQK	156
QY	89	ITVADLHLAGVNAENVGGPTVEELPGRRD-----SYVPRRGRLPDAAKKAP	137
Db	157	ISWADLFLTAGNVALLENSGFRFTGFAGGEDVWEPPDLVNWGDDEKAWLTHRPEALAKAP	216
QY	138	-----HNRDIFYRMGLTDKDIVAL-SGSHLSKAKH-----	166
Db	217	LGATEMGLIYVPEPDRHSNGEPLSAAAIATRAFTGNNGMNDEETVALINGHTLKGTHGAG	276
QY	167	-----PE-----BSGFDGANTRPDLKFDNSYFLELLKG	194
Db	277	PTSNVGPDPPEAPRIEEOGLGNASTYVGSVGADATISGLEVTWQTPQMSNYFEFELIFXY	336
QY	195	E-----SGGLLK-----LPTDRLALDDPEFRKRYVELIYAAD	224

DB	337	EMVQTRSPGALQIEFVADPEIIPDPDPSSKKRKPMLVTDLTLFDPDEFKISRFLND	396
OY	225	EDVEFKDYAESHKUJSELGFTPRSS--GPASKSDV	258
DB	397	PQAFNEAFARAFWKLTJHRDMGPKSRVIGPEVKEDL	432
		RESULT 11	
		US-08-459-499-13	
		; Sequence 13, Application US/08459499	
		; Patent No. 5871912	
		GENERAL INFORMATION:	
		APPLICANT: Heym, Beate	
		APPLICANT: Cole, Stewart T.	
		APPLICANT: Young, Douglas B.	
		TITLE OF INVENTION: Nucleic Acid Probes, Sequences, and Methods	
		TITLE OF INVENTION: for Detecting Mycobacterium Tuberculosis Resistant to Isonl	
		NUMBER OF SEQUENCES: 17	
		CORRESPONDENCE ADDRESS:	
		ADDRESSEE: Finegan, Henderson, Farabow, Garrett &	
		ADDRESSEE: Dunner	
		STREET: 1300 I Street, N.W.	
		CITY: Washington	
		STATE: DC	
		COUNTRY: USA	
		ZIP: 20005-3315	
		COMPUTER READABLE FORM:	
		MEDIUM TYPE: Floppy disk	
		COMPUTER: IBM PC compatible	
		OPERATING SYSTEM: PC-DOS/MS-DOS	
		SOFTWARE: Patent In Release #1.0, Version #1.3	
		CURRENT APPLICATION DATA:	
		APPLICATION NUMBER: US/08/459,499	
		FILING DATE: 02-JUN-1995	
		CLASSIFICATION: 536	
		PRIOR APPLICATION DATA:	
		APPLICATION NUMBER: US 07/875,940	
		FILING DATE: 30-APR-1992	
		PRIOR APPLICATION DATA:	
		APPLICATION NUMBER: US 07/929,206	
		FILING DATE: 27-MAY-1992	
		PRIOR APPLICATION DATA:	
		APPLICATION NUMBER: US 08/029,655	
		FILING DATE: 11-MAR-1993	
		ATTORNEY/AGENT INFORMATION:	
		NAME: Meyers, Kenneth J.	
		REGISTRATION NUMBER: 25,146	
		REFERENCE/DOCKET NUMBER: 03495.0110-03000 *	
		TELECOMMUNICATION INFORMATION:	
		TELEPHONE: 202-408-4000	
		TELEFAX: 202-408-4400	
		INFORMATION FOR SEQ ID NO: 13:	
		SEQUENCE CHARACTERISTICS:	
		LENGTH: 726 amino acids	
		TYPE: amino acid	
		TOPOLOGY: linear	
		MOLECULE TYPE: peptide	
		US-08-459-499-13	
		Query Match	17.2%; Score 257; DB 2; Length 726;
		Best Local Similarity	27.1%; Pred. No. 3e-19;
		Matches	91; Conservative 34; Mismatches 103; Indels 108; Gaps 10;
OY	31	APIMLRLAMHDAQY-DVNTRTGGANGSIRREBEETHGSNAGLKAIADLLEPIYAKH-PK	88
DB	97	AGLFLRMAMHGGAGTYSIDRGAGRGQORAPLNSWPDNYSLLKARLLMPPIQYTGOK	156
OY	89	ITYADHLQAGVAEVEVGGLPVEFIPIGRD-----SSVCPEGRLPDAKKGAP	137
DB	157	ISMADLFLTAGVVALENSGFRFTFGGAGREDYWEPPDLDVMMGDEKAMLTHTHPALAKAP	216

Db 100 PLEIRAMHAAGTYRIHDGSGAGGQRFAPLNSWPDNASLDAKARLLMPVKKYKGL 159
Qy 90 TVADHLQAGVAVEVGTGFTVEIFGRD-----SSVCPREGR 128
Db 160 SMADLIYFAGNCALIESMGFTFGFGRVDQWEPDEYWGKEATWLDERYSGRDLENP 219
Qy 129 L-----PDARKGAPHLRDIYRMGLTDKDIYAL-SGSHSLGKAH--- 166
Db 220 LAAVQMLIYVNEGPNGNDPMAAAVDIRETFRAMANDVETRALIVGHTFGKTHGAG 279
Qy 167 -----PE-----RSGFDGAWTRDPLKFDNSYFELLKG 194
Db 280 PADLVGPEPEAPLEQMGCLGKSSYGTGCKDAITSGIEVWWTNPTKWDNS-FLEILYG 338
Qy 195 ESEGLILKP-----TDKALLDDPEFRRYVELYA 222
Db 339 YEWELTKSPAGAQYAKDAGAGTIPDPGPGRSPTMLATDLSLAVDPIYERITRRL 398
Qy 223 KDEDVFEKDYAESHKLL--SELGFTPRSSGP-----AST 254
Db 399 EHPEELADEFAKAKMYKLIHDMGPVARYLGLPVKQTLMDQPVAVSHDLVGEAEIASL 458
Qy 255 KSDVSTAIVLAQSAVGVAVAAYVIAG 281
Db 459 KSOIRASGLTVSOLVSTAMAAASSFRG 485

RESULT 14
US-08-418-782-21

; Sequence 21, Application US/08418782
; Patent No. 5658733
; GENERAL INFORMATION:
; APPLICANT: Cockerill, Franklin R.
; APPLICANT: Kline, Bruce C.
; APPLICANT: Uhl, James R.
; TITLE OF INVENTION: Detection of Isoniazid Resistant Strains
; TITLE OF INVENTION: of M. Tuberculosis
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,782
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 150.141US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 740 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-418-782-21

Query Match 17.0%; Score 254; DB 1; Length 740;
Best Local Similarity 25.3%; Pred. No. 6.6e-19;
Matches 98; Conservative 36; Mismatches 115; Indels 138; Gaps 11;

Qy 32 PIMRLAMHDAGTYDVNTRTGANGSI-RYEEBYTHGSNAGLKIALIDLEPIKARH-PKI 89
Db 100 PLEIRAMHAAGTYRIHDGSGAGGQRFAPLNSWPDNASLDAKARLLMPVKKYKGL 159
Qy 90 TVADHLQAGVAVEVGTGFTVEIFGRD-----SSVCPREGR 128
Db 160 SMADLIYFAGNCALIESMGFTFGFGRVDQWEPDEYWGKEATWLDERYSGRDLENP 219
Qy 129 L-----PDARKGAPHLRDIYRMGLTDKDIYAL-SGSHSLGKAH--- 166
Db 220 LAAVQMLIYVNEGPNGNDPMAAAVDIRETFRAMANDVETRALIVGHTFGKTHGAG 279
Qy 167 -----PE-----RSGFDGAWTRDPLKFDNSYFELLKG 194
Db 280 PADLVGPEPEAPLEQMGCLGKSSYGTGCKDAITSGIEVWWTNPTKWDNS-FLEILYG 338
Qy 195 ESEGLILKP-----TDKALLDDPEFRRYVELYA 222
Db 339 YEWELTKSPAGAQYAKDAGAGTIPDPGPGRSPTMLATDLSLAVDPIYERITRRL 398
Qy 223 KDEDVFEKDYAESHKLL--SELGFTPRSSGP-----AST 254
Db 399 EHPEELADEFAKAKMYKLIHDMGPVARYLGLPVKQTLMDQPVAVSHDLVGEAEIASL 458
Qy 255 KSDVSTAIVLAQSAVGVAVAAYVIAG 281
Db 459 KSOIRASGLTVSOLVSTAMAAASSFRG 485

RESULT 15
US-08-228-662-7

; Sequence 7, Application US/08228662
; Patent No. 5688639
; GENERAL INFORMATION:
; APPLICANT: COCKERILL, FRANKLIN R.
; APPLICANT: KLINE, BRUCE C.
; APPLICANT: UHL, JAMES R.
; TITLE OF INVENTION: DETECTION OF ISONIAZID RESISTANT STRAINS
; TITLE OF INVENTION: OF M. TUBERCULOSIS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
; STREET: 3500 IDS CENTER
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,662
; FILING DATE: 18-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WOESSNER, WARREN D.
; REGISTRATION NUMBER: 30,440
; REFERENCE/DOCKET NUMBER: 150.123US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 740 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-228-662-7

Query Match 17.0%; Score 254; DB 1; Length 740;

PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
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Query Match 40.1%; Score 437; DB 21; Length 1157;
Best Local Similarity 69.6%; Pred. No. 2,1e-116;
Matches 612; Conservative 0; Mismatches 255; Indels 12; Gaps 1;

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QY 136 CATGATGCTGGACACTATGATGTGAACACAGAACTGTGTGTCATTAATTAATTAAGA 195
DB 229 CACGATGCTGGAACCTATGATGTCAATGGAAGACCGGTGACCTTAATGGCTCTATCAG 288
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Hybridisation assay; genetic mapping; gene expression control;
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metabolic pathway; promoter; termination sequence; ss.
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Query Match 40.1%; Score 437; DB 21; Length 1160;
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DB 172 GATGCTCCGTCCTCATGCTCCCAAGGAGTCCGCCCATCATGCTCCGCTCGCATG 231
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QY 196 TACGAGGAAGATACACCCATGTTCAATGCTGGCTTAAATTTGCTATTTATCTCTT 255
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DB 880 GACACACAGATTTGCGACAGAGTGCAGTGGGTGCGGTTTGCAGTTGCTGCTGCTTGTGCA 939
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RESULT 3
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 AC AAA68052;
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 XX 24-OCT-2000 (first entry)

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XX DE Pinus radiata peroxidase nucleotide sequence SEQ ID NO:145.
XX XX Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;
XX KW Pinus radiata; Monterey pine; ds.
XX OS Pinus radiata.
XX PN WO200022099-A1.
XX PD 20-APR-2000.
XX PF 06-OCT-1999; 99WO-NZ00168.
XX PR 09-OCT-1998; 98US-0169789.
XX PR 14-JUL-1999; 99US-0143811.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX PI Bloksberg LN, Havukkala JU;
XX DR WPI: 2000-317962/27.
XX XX
XX PT Novel polynucleotide encoding enzymes involved in lignin-biosynthetic
XX PT pathway useful for producing transgenic plants especially eucalyptus
XX PT and pine species having altered lignin content, composition and
XX PT structure -
XX PS Claim 1; Page 103; 213pp; English.
XX XX
XX CC The present invention describes isolated polynucleotides and proteins
XX CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H),
XX CC coumarate 3-hydroxylase (C3H), phenolase (PML), O-methyl transferase
XX CC (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase
XX CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4Cl),
XX CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),
XX CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,
XX CC caffeine acid methyl transferase, caffeoyl CoA methyl transferase,
XX CC coumarate CoA ligase, cytochrome P450 1XX1A, diphenol oxidase, flavanol
XX CC glucosyl transferase, flavanoid hydroxylase, and isoflavone reductase,
XX CC which are involved in the lignin biosynthetic pathway. The
XX CC polynucleotides can be used for modulating lignin content, lignin
XX CC composition and the structure of a plant, especially eucalyptus and pine
XX CC species, and for modifying the activity of an enzyme involved in lignin
XX CC biosynthetic pathway, and for producing a plant having altered lignin
XX CC content, composition and structure. They can be used for designing probes
XX CC and primers useful for detecting similar DNA and RNA sequences in any
XX CC organism and for PCR amplification. The lignin content can be efficiently
XX CC modified using the polynucleotides. AAA67908 to AAA68201 and AAB16341 to
XX CC AAB16449 represent polynucleotide and protein sequences used in the
XX CC exemplification of the present invention.
XX SQ Sequence 1080 BP; 287 A; 228 C; 268 G; 297 T; 0 other;
  
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Query Match 27.9%; Score 303.6; DB 21; Length 1080;
 Best Local Similarity 63.4%; Pred. No. 1.1e-77;
 Matches 465; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

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QY 16 GCGATGCGCGCTCCGCTGTCGACCGCCGAGTACCTCCGCCAGTGCACAGGCGCGCCG 75
DB 73 GTGAAGGCTTTATCCCAACCGTAAAGGAGTGAACAAGGCTGCCATGACAAATGCAAGAG 132
QY 76 GCGTCCGTCGCTCATGCTCCCAAGGAGTCCGCCCATCATGCTCCGCTCGCATG 135
DB 133 AAGCTCCGAGCTCTCATTTGCAAGAGAACTGTGGCGGATCATGTTGTAATGCAATGG 192
QY 136 CATGATGCTGCGACCTATGATGTGAACACAGAACTGCTGTCGAATGTTCAATTA 195
DB 193 CACAGCGCTGGAGTTTACGATGTCAAGACCAAGCGGAGGCGCTTGGAGCATGAGA 252
QY 196 TACGAGGAAGATACACCCATGTTCAATGCTGGCTTAAATTTGCTATTTATCTCTT 255
  
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Db 253 TATGGGGCCGAGCTTCCCAAGCTGCTTAACATGTTGCTGACATTCGACATTAAGCTCTCTG 312
QY 256 GAGCCTATTAAAGCGAGCATCCAAAGATTACATATGACAGCTTGCATCTGCGCGA 315
Db 313 GAGCCAAATCAAGGAACAGTATCCCATTAATCATCTGATGCTTATGATGAGTGGGTGGT 372
QY 316 GTAGTTGCAAGTTGAAGTCAACCGGGGGTCCAAACCGTTGAGTTCATCCCTGGAAGACGTGAT 375
Db 373 GTGGTGGCTGTTGAAAGTGAACCGGGGGGACCTGACATTCCTGATCCCTGGAAGAGAAC 432
QY 376 TGTGAGTTGTGTCCTCCGAGAGAGCTTCTGATGCTAAGAAAGGTGACACCATCTA 435
Db 433 AAGCCTGAGACCTCCAGAAAGAGCCCTTCTGATGCTAACAAGAGACCTGATCATCTG 492
QY 436 AGGACATCTTTTATGAAATGGGGTTACAGACAAAGATATTTAGACATCTATCTGGGGGG 495
Db 493 AGGATGTTTGTGTCATAGGGGTTGAAATGATAGAAATTTGGGCTTGTCTGGGTGCC 552
QY 496 CACAGCCTGGGAAAGGCGCATCTGAAAGGTCTGGGTTTGACGGTGCATGACCTGTCGAC 555
Db 553 CACACCTTGGGGAGATGCCAAGAGAGATCTGTTTGAAGAGACCATGACCTCTAC 612
QY 556 CCTGAAATTTGACACATCATCTTCTTGTGAGCTACTGAAAGGGGAAATCTGAGGGTCT 615
Db 613 CCCCTTATCTTGTGACAACTCTTACTTACAGAGCTTGTGACTGAGAGAGAAAGGCGCTG 672
QY 616 CTGAAGCTCCCTACTGATTAAGCATTTGTGATGATCTGAAATTTGACGCTATGTGAG 675
Db 673 CTTCAGTTGCCATCTGATTAAGCATGCTGCTGATGATCTTGTGACAGTTATGTTTCA 732
QY 676 CTTTATGCAAGAGATGAGATGTTTCTTCAAGSACTAGCGTAATCACAACAAAACCT 735
Db 733 AAGTATGACAGAGACAAAGACGTTCTTCTGCTGACTATGCGAAGCTCACCTGAAGCTT 792
QY 736 TCTGAATCTGGCTT 749
Db 793 TCTGAATCTGGCTT 806

RESULT 4

AAV23904
ID AAV23904 standard; DNA; 1229 BP.
AC AAV23904;
XX 31-JUL-1998 (first entry)
DT
XX
DE Plant POX enzyme DNA sequence.
XX
KW Lignin biosynthetic pathway; eucalyptus; pine; transgenic plant;
KW Lignin content; tree processing; cellulose fibre; ss.
XX
OS Pinus radiata.
XX
PN WO811205-A2.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-NZ00112.
XX
PR 11-SEP-1996; 96US-0713000.
XX
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Bloksberg LN, Grierson AW, Havukkala JU;
XX
DR WPI: 1998-207374/18.
XX
XX Sequences useful for modification of plant lignin content or
XX structure - from Eucalyptus grandis (eucalyptus) and Pinus radiata
XX (pine) are associated with lignin biosynthesis pathway, useful e.g.
XX in paper industry

XX
PS Claim 1; Page 68-69; 82pp; English.
XX
CC This sequence represents a fragment of the POX enzyme coding sequence. It
CC is an example of a DNA sequence of the invention, which are from
CC Eucalyptus grandis (eucalyptus) and Pinus radiata (pine) associated with
CC the lignin biosynthesis pathway. Constructs containing the DNA sequences
CC can be used to produce transgenic plants or plant cells, especially woody
CC plants e.g. eucalyptus or pine species but also e.g. monocotyledons or
CC dicotyledons; by stably incorporating the constructs into the plant
CC genome. The lignin content or structure, or activity of a specific enzyme
CC in the plant, can therefore be modulated. Reductions in lignin content or
CC changes in composition are useful in tree processing for paper. High
CC lignin content results in energy- and chemical-intensive separation
CC methods in order to obtain the pure cellulose fibre required. Reductions
CC in lignin content may also be useful for forage crops, whilst increases
CC or changes in composition may be desirable to increase the mechanical
CC strength of wood, change its colour or increase its resistance to rot.
CC The sequences are also useful as probes to isolate DNA sequences encoding
CC enzymes involved in the lignin biosynthesis pathway from other plant
CC species.
XX

Sequence 1229 BP; 342 A; 256 C; 292 G; 339 T; 0 other:

Query Match 27.9%; Score 303.6; DB 19; Length 1229;
Best Local Similarity 63.4%; Pred. No. 1.2e-77;
Matches 465; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

QY 16 GCATGAGCGGCTCGGCTGAGACGCGGAGTACCTGCGCCAGCTGACAGAGGCGCGCGC 75
Db 222 GTGAAGCTTTATCCACCGCTAAGAGAGAGTACAAAGCTCCATTGACAAATGCAAGG 281
QY 76 GCTTCCTGTCCTCATGCTCCAGAGGATGCGCCCATCATGCTCGCTGCATG 135
Db 282 AAGCTCCGAGCTCTCATTTGACAGAAAGACTGTGGCCGATCATGTTGAAATGCAATG 341
QY 136 CATGATGCTGGGACCTATATGTGAACACAAAGACTGTGGTGGTCAAAATGTTCAATTGA 195
Db 342 CACAGGCTGGGAGCTTACATGATGCAACCAAGAGCGGCGCTTGGGACGTGGA 401
QY 196 TACGAGAAAGATGACACCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255
Db 402 TATGGGGCCGAGCTTCCCAACGCTGCTAACAAGTGTGCTGACATGCGATTAAGCTCTG 461
QY 256 GAGCCTATTAAAGCGAGCATCCAAAGATTACATATGACAGACCTTACATGCTGCGCGA 315
Db 462 GAGCCAAATCAAGGAACAGTATCCCATTAATCATCTTATGCTGATGCTGATGCTGCT 521
QY 316 GTAGTTGCAAGTTGAAGTCAACCGGGGGTCCAAACCGTTGAGTTGATCCCTGGAAGCTGAT 375
Db 522 GTGGTGGCTGTTGAAGTGAACCGGGGGACCTGACATTCGTTCCATCTGGAAGAGAAC 581
QY 376 TGTGAGTTGTGTCCTCCGAGAGAGCGCTTCTGATGCTAAGAAAGGTGACACCATCTA 435
Db 582 AAGCCTGAGACCTCCAGAAAGAGCGCGCTTCTGATGCTAACAAGAGACCTGATCATCTG 641
QY 436 AGGACATCTTTTATGAAATGGGGTTAACAGACAAAGATATTTAGACATCTATGCGGGG 495
Db 642 AGGATGTTTGTGTCATAGGGGTTGAATGATAGAAATTTGGCTTGTGCTGCTGCTGCT 701
QY 496 CACAGCCTGGGAAAGGCGCATCTGAAAGGTGTGGGTTTGAACGCTGATGACCTGTCGAC 555
Db 702 CACACCTTGGGAGATGCAACAAAGAGAGATCTGTTTGAAGGACCTGACCTCTAAC 761
QY 556 CCTGAAATTTGACAACTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
Db 762 CCCCTTATCTTGTGACAACTCTTACTTACAGAGCTTGTGCTGCTGCTGCTGCTGCTGCT 821
QY 616 CTGAAGCTCCCTACTGATTAAGCATTTGTGATGATCTGAAATTTGCAAGCTATGTGAG 675
Db 822 CTTCAGTTGCAATGATTAAGCACTGCTGCTGATCTAGTTTGCAGTTTATGTTTCA 881
QY 676 CTTTATGCAAGAGATGAGATGTTTCTTCAAGAGACTACGCTGAATTCACACAAAACCTT 735

[illegible]

Db	222	GTGAAGGCTTATCCACCGTAAAGGAGATGATCAAGGCTGCATTGACAAATATGCAAGG	281
Qy	76	GCCTTCGGTCCCTCATCGCTCCACAGGAGATGCGCCCATCATGTCGCGCTGCATGG	135
Db	282	AAGCTCCGAGCTCTCATGTGCAAGAGAACATGTGCGCGATCATGTTCGAATGGCATGG	341
Qy	136	CATGATGCTGCGACCTATGATGTGAACAACAAGAACGTGGTGGTGCAAAATGGTCAATTAGA	199
Db	342	CACACGCGCTGGACTTACGATGTCAAGACCAAGACCGGAGGGCCCTTCGGACGATGAGA	401
Qy	196	TACAGAGGAAGATACACCCATGTGTTCAATAGTCTGGCTTAAAAATTTGCTATTGATCTCTT	255
Db	402	TATGGGGCGGACCTTGCACAGGTGTCTTAACAGGTGTGGACATCGAGTAGTAGGCTCTCG	461
Qy	256	GAGCCTATTAAAGCCAGCATATCCAAAGATTTATATGACAGCTTCATACGCTTGGCGGA	315
Db	462	GAGCCATATCAGAGAACAGTTCCTCCCATATATCATATGCTGACCTTATATCAGTTGGCTGGT	521
Qy	316	TATGTTGCAAGTTGAAGTACCGCGGGGGTCCAAACGTTGAGTTCATCCCTGGAAGACGTAT	379
Db	522	GTGTGGGCTGTGTAAGTACCGGGGGACCTGATATTCGGTTCCATCCTGGGAAGGAAGAC	581
Qy	376	TGTGATGTTTGTCCCGTGAAGAGACGCTTCTGATGCTTAAGAAAGTGCACCATCTA	435
Db	582	AAGCCTGAGCCCTCGAAGAAAGGCGCCCTTCTGATGTACAAAAGGACCTGATCATCTG	641
Qy	436	AAGGACATCTTTATATGAGATGGGGTTAACAAGACAAAGATATTGTAGCACTATCTGGGGGG	499
Db	642	AAGGATGTTTTTGGTACATGGGGTTGATGATTAAGGAAATTTGGGCTTGTCTGGTGC	701
Qy	496	CACAGCCTGGGAAAGGCGCATCTGTGAAAGTCTGGGTTTGAAGGTGATGAGTACCTGAGAC	555
Db	702	CACACCTTGGGGAGATGGCACAGAGAGATCTGTGTTTTGAAGACCATGAGCACTCTAAC	761
Qy	556	CCTCTGAAATTTGACACTCATACTTCTTGAAGCTACTGAAGGGGAATCTGAGGCTTT	615
Db	762	CCCTTACTTCTTGACACCTTACTTACAGAGCTTGTGACTGGAGAAAGAGCGCTG	821
Qy	616	CTGAAGCTCCCTACGATTAAGGCAATGTGTGATGATCTGAAATTTGCACCGCTATGTGAG	675
Db	822	CTTCACTTGGCCATGATTAAGGCACTGCTTCTGATCTCTGATTGTCAGTTATGTTCAG	881
Qy	676	CTTTATGCAAAAGATGAGATGTTTTCTTCAAGGACTACGCTGAAATCACACAAAAAATT	735
Db	882	AAGTATGCAAGAGAGAGAGAGCGCTTCTTCTTGTGACTATGGGAGAGCTCACCTGAGCTT	941
Qy	736	TCTGACTTGGCTT 749	
Db	942	TCTGAACTTGGGT 955	
RESULT 6			
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ID	AAA67992 standard; DNA; 1229 BP.		
AC	AAA67992;		
XX			
XX	24-OCT-2000 (first entry)		
DE	Pinus radiata peroxidase nucleotide sequence SEQ ID NO:85.		
XX			
KW	Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;		
KW	Pinus radiata; Monterey pine; ds.		
XX			
OS	Pinus radiata.		
XX			
PN	WO200022099-A1.		
PD	20-APR-2000.		
XX			
PF	06-OCT-1999; 99WO-NZ00168.		
PR	09-OCT-1998; 98US-0169789.		

PR 18-MAY-1999;	990S-0134768.
PR 19-MAY-1999;	990S-0134941.
PR 20-MAY-1999;	990S-0135124.
PR 21-MAY-1999;	990S-0135353.
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PR 25-MAY-1999;	990S-0136021.
PR 27-MAY-1999;	990S-0136392.
PR 28-MAY-1999;	990S-0136782.
PR 01-JUN-1999;	990S-0137222.
PR 03-JUN-1999;	990S-0137528.
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PR 23-JUL-1999;	990S-0145145.
PR 23-JUL-1999;	990S-0145218.
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PR 26-JUL-1999;	990S-0145276.
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PR 21-OCT-1999;	990S-0160815.
PR 22-OCT-1999;	990S-0160980.
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PR 22-OCT-1999;	990S-0160989.
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PR 25-OCT-1999;	990S-0161405.
PR 25-OCT-1999;	990S-0161406.

[illegible]

Query Match	24.7%;	Score 269.4;	DB 21;	Length 982;
Best Local Similarity	61.9%;	Pred. No. 9.2e-68;		
Matches 445;	Conservative 0;	Mismatches 271;	Indels 3;	Gaps 1,

QY	34	GTGAGCGCCGAGTACCTGCGCCAGGTGCACAGGGCGGCGCGCTTCGTCGCCATC	93
Db	36	GTGACCGGAAGATTACAAAGAGCGTGTGTAGAAATGTCAGAGAGGAAGCTACAGAGTTTATC	95
QY	94	GCGTCCAAAGGGATGCGCCCCCATCATGCTCCCGCTCGCATGGCATGTAGATGGCGACCTAT	153
Db	96	GCTGAGGAAGATGTGACACCATCATGTGTGCTGACTCGCATGTGGCACTGTGCTGGAACTTC	155
QY	154	GATGTGAACACAAAGAACCTGTGTGTGTGTGCAAAATGTTCAATTAGATACGAGGAAGACTACAC	213
Db	156	GATTGTGCATCAATGAAGACACGTGAGGTGCATTCCGAACCAATGAGGTTTGAACGCGTGACCAAGCT	215
QY	214	CATGGTTCAAAATGCGGCTTAAAAATTGCTATTGATCTCCGTGAGCCTATTAAAGCAAG	273
Db	216	CATGAGGCCAACAGTGGTATCCACATTCCTCTTATGTTGTGTGAGACCCCATCAGGAGACAA	275
QY	274	CATCCAAAGATTACATATGACAGACCTTCATCAGCTTGCCGAGTAGTTGCAGTTGAAGTC	333
Db	276	TTCCCTACCACTCTTTTGTGTGATTTCCATAGCTTGTGTGTGTGTGTGGCGCGTTGAAGTT	335
QY	334	ACCGGGGGTCCACCGTTGATGTATCCCTCGTGAAGAGGTGATGTGTGATGTTGTGCCCGT	392
Db	336	ACTGTGTGGCCTTGACATTCCTTTCCACCCTTGAAGAGAGCAAGCCCAACCACTTCCA	395
QY	394	GAAGACGCGCTTCTGTGATCTAAGAAAAGTGCACACATCTTAAGGAGACATCTT--TTAT	450
Db	396	GAGGGTGTCTTCCGTGATGCTACCAAGGGTGTGACCATTGGAAGATGTTCTTGCTAAG	455
QY	451	CGAATGGGGTTAACAAGCAAAAGATATTGTAGCACTATCTGGGGGCAACACCTGGGAAG	510
Db	456	CAGATGGGCTTATCTGCAAAAAGCAATTGTGCTTATCTTGGTGCGCCACACTCTGGGAGCA	515
QY	511	GCGCATCTCTGAAGAAGTCTGGGTTTGACGGTGCATGACACTGCACTCTGAATTTGAC	570
Db	516	TGCCACAAGGATATGAGTGTGCGCTTGGAAGTGCATAGCAATCAACCTCTTAATCTTGAC	575
QY	571	AACATCATCTTCTTGTGAGCTACTGAAGGGGGAATCTGAGGCTCTTGTGAAGCTCCTACT	630
Db	576	AACCTTTACTTCAAGGAAGACTTTAGGGGGAAGGAAGAGGCCCTTCTCAGCTGTGTCTCT	635
QY	631	GATTAAGGCAATGTTGATGATCTGAAATTTGACAGCTATGAGAGCTTTATGCAAAAGAT	690
Db	636	GACAAAGACATATTGAGAGACCGCTGTTTCCGTCTTGTGTGCAAGAAATACGCTGCTGAT	695
QY	691	GAGGATGTTTCTTCAAGGACTACGCTGATATCACCAAAAACTTCTGAACTTGGCTT	749
Db	696	GAAATGCGCTTTTTCGCTGATTTAGCTGTGAGGCCCAACGAAGAGCTTTCTGTGAGTGTGGCTT	754

RESULT	ID	SEQ	DESCRIPTION
8	AAC48375	1110	standard; DNA, 1110 BP.
XX	AC		
XX	AAC48375;		
XX	18-OCT-2000		(first entry)
XX			
DE	Arabidopsis thaliana		DNA fragment SEQ ID NO: 57252.
XX	Hybridisation assay;		genetic mapping; gene expression control;
XX	protein identification;		signal transduction pathway;
KW			

KW	metabolic pathway; promoter; termination sequence; ss
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 200EP-0301439.
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PR	25-MAR-1999; 990S-0121825.
PR	05-MAR-1999; 990S-0122180.
PR	09-MAR-1999; 990S-0123548.
PR	23-MAR-1999; 990S-0125788.
PR	25-MAR-1999; 990S-0126264.
PR	29-MAR-1999; 990S-0126785.
PR	01-APR-1999; 990S-0127462.
PR	06-APR-1999; 990S-0128234.
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PR	30-APR-1999; 990S-0132407.
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PR	14-MAY-1999; 990S-0134218.
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PR	27-MAY-1999; 990S-0136392.
PR	28-MAY-1999; 990S-0136782.
PR	01-JUN-1999; 990S-0137222.
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PR	18-JUN-1999; 990S-0139750.
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Query Match 24.7%; Score 269.4; DB 21; Length 1110;
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OY 94 GCCTCCAGGAGATGCCGCCCATCATGCTCGCTCGCATGAGTCAGTGGACACTAT 153
DB 225 GCTGAGAGAACTGTGACACCATCATGTCGACATGCGCATGCGACTTGTGAACTTC 284
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DB 345 CATGAGGCCAAGAGTGTATCCACATGTCTTATAGTTGTGACCCATCAGGAGCA 404
OY 274 CATCCAAAGATTACATATGACAGACCTTATCATGACTTCCGCGAGTAGTGCATGAAGTC 333
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OY 334 ACCGGGGGTCCAAAGCTGAGTTCAATCCCTGGAAGCGTAGTTCGATGTTGCCCGT 393
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KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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Query Match 24.7%; Score 269.4; DB 21; Length 1122;
Best Local Similarity 61.9%; Pred. No. 9.9e-68;

Matches 445; Conservative 0; Mismatches 271; Indels 3; Gaps 1;

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DB 236 GCTGAGAGAACTGTGACCCCATCATGCTGCTCGCATGAGCTGGCACTAT 295
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DB 416 TTCCTTACCATCTCTTTGCTGATTTCATCATGCTTGCTGCTGCTGCTGCTGAAGTT 475
QY 334 ACCGGGGGTCAGAGCGTTGATTCATCCCTGAGAGACGATTCATGTTGTCCCGT 393
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QY 394 GAAGACGCGCTTCGTGATGCTAAGAAAGGTGCACCACATCTAAGGAGACATCTT---TTAT 450
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DB 716 AACTTACTTCAAGAACTCTTGACGAGAGAAAGAGGCTTCTTCACTTGTCTCT 775
QY 631 GATTAAGCATTTGTTGATGATCTGAAATTTTCAGCCTATGTGAGCCTTTATGCAAGAT 690
DB 776 GACAAAGCACATTTGAGACGACCTGTTTCCGCTTGTGAGAAATACGCTGCTGAT 835
QY 691 GAGGATGTTTTCTCAAGGACTAGCTGATATCAACACAAAACCTTGTGAATTTGGCTT 749
DB 836 GAAGATGCTTTTTCGATTACGCTGAGGCGCACATGAACCTTTCTGAGCTTGGGTT 894

RESULT 11

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AC AAC37495;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 17589.

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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Best Local Similarity 61.9%: Pred. No. 9.9e-68;
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DB 236 GCTGAGAGAACTGTGCACCCATCATGTCCGACTGCGACACTGCTGGAACTTTC 295
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QY 511 GCGCATCCGAAGGTCGTGGGTTGAAGGTCATGAGACTCGTACCTCTGAATTTGAC 570
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QY 571 AACTCATACTTCTTCTAGCTACTGAAGGGGAATCTGAGGGTCTTCTGAAGCTCCCTACT 630
DB 716 AACTCTTACTTCAAGAACTCTTGAGCGAGAGAAAGAGGCTTCTTCACTTGTCTCT 775
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RESULT 12
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AC AAC48374;
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XX 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57248.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
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Query Match 24.7%; Score 269.4; DB 21; Length 1213;
Best Local Similarity 61.9%; Pred. No. 1e-67; Mismatches 271; Indels 3; Gaps 1;
Matches 445; Conservative 0;

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DB 328 GGTGAGAAAGACTGTGCACCATCATGTGCTGCATGTCGATGTCATGCTGGAACTTTC 387
QY 154 GATGTGAACACAGACTGTGTGCAATGTTCAATTAGTATAGGAGGAGATACACC 213
DB 388 GATTGTCAATCAAGAGCTGAGGTCCATTGCAACAAATGAGTTTGAGCTGACCAACT 447
QY 214 CATGTTCAATGCTGGCTTAAATTTGCTATTTGATCTCCTTGAGCTTATTAAGCGAAG 273
DB 448 CATGAGCCCAACAGTGTATCCATTTGCTCTTAGTTTGTGGACCCCATGAGGAGCA 507
QY 274 CATCAAAAGATTACATATACAGACTTCATCAGCTTGCAGGAGTAGTTGACGTTGAAGTC 333
DB 508 TTCCCTACCATCTCTTTGCTGATTTCCATCAGCTTGTGCTGTGCGCTGGAATTT 567
QY 334 ACCGGGGTCCCAACGTTGATGTTATCCCTGGAAGACGTGATTCCTCAGATTGTCCTCCCT 393

Db 568 ACTGATGGCCCTGCATCTTCCTTCCACCCCTGGAGAGAGACAGCCCAACCACTTCCA 627
Oy 394 GAAGAGACGCTTCCTGCATGCTAGAGAAAGGTGCACACATCTAAGGACATCTT---TTAT 450
Db 628 GAGGCGTGTCTTCGATGCTTACCAAGGGTTTGACACATTTGAGATGTGCTTTGGCTAAG 687
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Oy 691 GAGGATGTTTCTTCAAGGACTACGCTGATCATCACAAAAAATTCTGAGCTTGCGCT 749
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RESULT 13
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XX AAC34745;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 7736.

DE Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

PN EPI033405-A2.

PD 06-SEP-2000.

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PF 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161362.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 24.7%; Score 269.4; DB 21; Length 1216;
Best Local Similarity 61.9%; Pred. No. 1e-67;
Matches 445; Conservative 0; Mismatches 271; Indels 3; Gaps 1;

QY 34 GTGAGCGCCGACCTGCGCCAGCTGCGACAGGAGCGCCGCGCCCTTCGTCGCCCTCATC 93
DB 269 GTGAGCGAGATTACAGAGAGGCTGTGAGAAAGTGCAGAGAGAGAGCTCAGAGGTTGATC 328
QY 94 GCCTCCAGGAGATGCGCCCATCATGCTCCGCTTCGATGAGCATGATGCTGGACCTAT 153
DB 329 GCTGAGAGAACTGTGCACCCATCATGTCGCCATGCGATGCGACTTCCTGGAACCTTTC 388
QY 154 GATGTGACACAGAACTGGTGTGCAATGTTCAATTAGATAGAGAGAGATACACC 213
DB 389 GATTGTCAATCAAGACTGAGGTCATTCCGAAACATGAGGTTTGACCTGAGCAACT 448
QY 214 CATGTTCAATCTGCGCTTAAATTCATTTGATCTCCTTGAGCCATTATAAGCGAAG 273
DB 449 CATGAGCCCAAGGTGATCCCATGCTCTTAGTTTGTGACCCCATCAGGAGCA 508
QY 274 CATCAAAAGATTACATATGACACTTCATCAGCTTCCGGAGTGGTACAGTTGAAGTC 333
DB 509 TTCCCTACCATCTCTTTGCTGATTTCCATCAACCTTGCTGTTGGCCCTGAAGTT 568
QY 334 ACCGGGGGTCCACCGTTGAGTTGATCCCTGGAAAGCGATTCGTCACTTGTCCCGT 393
DB 569 ACTGTGGCCCTGACATTCCTTTCACCCCTGGAAAGAGAGAACCCCAACCCACTCCA 628
QY 394 GAAGAGCGCCCTTCGATGTAAGAAAGTGCACCCATCTAAGGACATCTT--TTAT 450
DB 629 GAGGTCGTCTTCTATGCTACCAAGGTTGTGACCATTTAGAGATGTCTTTGCTAAG 688
QY 451 CGAATGGGTTAAACAGAAAGATATTGACACTATCTGGGGGACACACCTGGAAAG 510
DB 689 CAGATGGGCTTATCTGACAAAGACATTGGCTTATCTGGTGCCACACTCTGGAGCA 748
QY 511 GCCCATCTGAAAGCTGTGGGTTTGACGGTGCATGACACTGACCCCTGAAATTTGAC 570
DB 749 TGCACAGAGATAGTCTGTGGCTTGAAGGTGATGACATVCAACCCCTTAATCTTGAC 808
QY 571 AACTCATCTTCTTGTAGCTACTGAAGGGGAATCTGAGGAGCTTCGAGCTCCCTACT 630
DB 809 AACTCTTACTTCAAGAACTCTTGACGGAGAGAAAGAGCCCTTCTCAGTTGTCTCT 868
QY 631 GATAGGCAATGTTGATGATATCTGAAATTCGACGCTATGTGAGACTTATGCAAGAT 690
DB 869 GACAAAGCACTATGAGACACCTGTTTCCGCTTTGGTGAAGAAATACCTGCTCAT 928
QY 691 GAGGATGTTTCTTCAAGAGACTAGCTGAATCAACCAAAAACCTTGTGAATTTGGCT 749
DB 929 GAAGATGCTTTTCTGCTGATTAAGCTGAGGCCACATGAACCTTTCGAGCTTGGGTT 987

RESULT 14
AAA68085
ID AAA68085 standard; DNA; 409 BP.
XX
AC AAA68085;
XX
DT 24-OCT-2000 (first entry)
XX
DE Pinus radiata peroxidase nucleotide sequence SEQ ID NO:178.

XX plant; lignin: lignin biosynthetic pathway; Eucalyptus grandis;
KM Pinus radiata; Monterey pine; ds.
XX
OS Pinus radiata.
XX
PM WO200022099-A1.
XX
PD 20-APR-2000.
XX
PF 06-OCT-1999; 99WO-NZ00168.
XX
PR 09-OCT-1998; 98US-0169789.
PR 14-JUL-1999; 99US-0143811.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Bloksberg LN, Havukkala IU;
PI
DR WPI; 2000-317962/27.
XX
XX Novel polynucleotide encoding enzymes involved in lignin-biosynthetic
PT pathway useful for producing transgenic plants especially eucalyptus
PT and pine species having altered lignin content, composition and
PT structure -
XX
PS Claim 1; Page 112; 213pp; English.
XX
XX The present invention describes isolated polynucleotides and proteins
CC encoding and representing the enzymes cinamamate 4-hydroxylase (C4H),
CC coumarate 3-hydroxylase (C3H), phenolase (PML), O-methyl transferase
CC (OMT), cinamyl alcohol dehydrogenase (CAD), cinamoyl-CoA reductase
CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4CL),
CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),
CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,
CC caffeic acid methyl transferase, caffeoyl CoA methyl transferase,
CC coumarate CoA ligase, cytochrome P450 1X1A, diphenol oxidase, flavanol
CC glucosyl transferase, flavonoid hydroxylase, and isoflavone reductase,
CC which are involved in the lignin biosynthetic pathway. The
CC polynucleotides can be used for modulating lignin content, lignin
CC composition and the structure of a plant, especially eucalyptus and pine
CC species, and for modifying the activity of an enzyme involved in lignin
CC biosynthetic pathway, and for producing a plant having altered lignin
CC content, composition and structure. They can be used for designing probes
CC and primers useful for detecting similar DNA and RNA sequences in any
CC organism and for PCR amplification. The lignin content can be efficiently
CC modified using the polynucleotides. AA67908 to AA68201 and AB16341 to
CC AB16449 represent polynucleotide and protein sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 409 BP; 101 A; 86 C; 112 G; 110 T; 0 other;

Query Match 19.4%; Score 211.6; DB 21; Length 409;
Best Local Similarity 73.1%; Pred. No. 3.4e-51;
Matches 285; Conservative 0; Mismatches 104; Indels 1; Gaps 1;

QY 303 TCAGCTTCCGCGAGTAGTTCAGTGAATGACCGGGGTCCACCGGTGATGATCC 362
DB 20 TCAGCCGGGTGTAGTTCAGTTCAGTTCAGGAGGTCCACATTTGATGTC 79
QY 363 TGAAGAGCTGATTCGTGCTGTCGCCGTGAGAGACGCTTCGTGATGATGAG 422
DB 80 TGTGCTGAGTATGATCTGTCATGACACGAGAGAGCGCTTCGTGATGAGAG 139
QY 423 TGCACACATCTAAGGAGATCTTTATGATGGGTTTAACAGCAAGATATGTAC 482
DB 140 TTTCAACACCTAAGGAGATCTTTATGATGGGCTTATGACAGATATGTTCC 199
QY 483 ACTATCTGGGGGACAGC-CTGGGAAAGCGCATCTGAAGGCTTGGGTTGAGCGTG 541
DB 200 TCTTTCTGAGGCGACACCATTTGGGAAAGACATCCAGAAAGTGATGATGAG 259

QY 542 CATGACTGCTGACCTCTGAAATTTGACACTCATCTTTCTTGACTACTGAAGGGG 601
DB 260 CATGGACCGACGACGCTCTGAAATTTGATGATGATTTCTGAGCTTCAAGGCG 319
QY 602 AATCTGAGGGTCTCTGAGGCTCCCTACGATTAAGGCATTTGATGATCTGATTC 661
DB 320 AGCTGAAAGATTAATCTCCATTTGCTGAGGACAAATGCTTGGTAGGATCCAGTTCC 379
QY 662 GACGCTATGAGCTTTATGCAAGGATG 691
DB 380 GCCCTATCTGATCTTTATGCCAAGATG 409

RESULT 15
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ID AAC51668 standard; DNA; 687 BP.
XX
AC AAC51668;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 69352.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PM EP1033405-A2.
PM
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
PF 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 04-JUN-1999; 99US-0137502.

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Query Match 19.2%; Score 209.2; DB 21; Length 687;
 Best Local Similarity 63.4%; Pred. No. 2.3e-50;
 Matches 354; Conservative 0; Mismatches 195; Indels 9; Gaps 2;

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OY 337 GGGGTCACACGTTGAGTTTCATCCCTGAGACGTAATGCTCAAGTTTGTCCCGTGAA 396
    || || || || || || || || || || || || || || || || || || || || ||
Db 2 GGTGACCTGACATGTCGTTCCTCCGGAGAAAGGATTCAAATGTCGCCCAAGGAA 61
    || || || || || || || || || || || || || || || || || || || || ||
OY 397 GGAGCCCTTCGATGCAAGAAAGGTGACCAACATCAAGGACATCTTTATATGAAATG 456
    || || || || || || || || || || || || || || || || || || || || ||
Db 62 GGAAGACTTCGATGACCAAGATTTCCACATCTCAGAGATGTCCTTACCGCATG 121
    || || || || || || || || || || || || || || || || || || || || ||
OY 457 GGGTTACAGACAAAGATATTGTAGCACTATCTGGGGGGGACAGCCCTGGGAAAGCGCAT 516
    || || || || || || || || || || || || || || || || || || || || ||
Db 122 GGACATATCGATTAAGATATTGTGGCACTCTCAGGGGGGTCACTCTGGGAAGGGCTCAC 181
    || || || || || || || || || || || || || || || || || || || || ||
OY 517 CCTGAAGGTCGTGGGTTGACGCGTCATGACCTGACCCCTGAAATTTGACAACATCA 576
    || || || || || || || || || || || || || || || || || || || || ||
Db 182 CCAGAGAGGTGACGCTTGATGACATGACCCCAAGAGCCGCTGAAGTTTGACAACCTCC 241
    || || || || || || || || || || || || || || || || || || || || ||
OY 577 TACTTCTTGACCTACTGAAAGGGGAATCTGAGGCTTCTGTAAGCTCCTACTATAG 636
    || || || || || || || || || || || || || || || || || || || || ||
Db 242 TACTTCGTGAACTGCTGAAGAGAAATCAGAGGGCTGTGAAACT-TCAACTGACAAG 300
    || || || || || || || || || || || || || || || || || || || || ||
OY 637 GCATTGTTGATGATCTGTAATTTGACGCTATGTGAGCTTTATGCAAAAGATGAGAT 696
    || || || || || || || || || || || || || || || || || || || || ||
Db 301 ACCTTATTGGAAGACCCGAGTCCGTCCTCTTGTGAGCTTTATGCAAAAGATGAAAGA 360
    || || || || || || || || || || || || || || || || || || || || ||
OY 697 GTTTCCTCAAGGACTACGCTGAATCACAACAAAACCTTCTGAACCTGGCTTCAACCCA 756
    || || || || || || || || || || || || || || || || || || || || ||
Db 361 TGCATTCTTAGAGACTACGCGGAATCCACAAGAAACTCTNTGAGCTTGTGTTCAACC 420
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OY 757 CGGACAGTGGGCCAGCACTCTCAAAAATCAGATGTTCAACTGCTGTGTACTTGCACAG 816
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Db 421 CCAACTCCTCAACAGGCAAAAAGCAGT-----TTGACAGACGACCACTTCTGACCAA 472
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OY 877 TCCAAAGAGAGCAAGTAA 894
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Db 533 CCGAAGAGGTGAAGTAA 550
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Search completed: October 25, 2002, 16:23:23
 Job time : 225 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 15:52:06 ; Search time 1720 Seconds
(without alignments)
8545.456 Million cell updates/sec

Title: US-09-870-501-2

Perfect score: 1089
Sequence: 1 cttcaggtcgtccgcgat.....gaataaaaaaaaaaaaaa 1089

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estchum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
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8: em_hic:*
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15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	664	61.0	664	9	AV945933
7	662	60.8	662	9	AV929644
8	661	60.7	661	9	AV942984
9	660.4	60.6	666	9	AV937941
10	656.4	60.3	677	9	AV940735
11	639.2	58.7	863	10	BF254606 HVSNEF000
12	632.4	58.1	654	9	AV938146
13	631.4	58.0	652	9	AV934694
14	625.4	57.4	630	9	AV940226
15	623.4	57.2	630	9	AV909151
16	617.4	56.7	630	9	AV943215
17	617	56.7	665	9	AV922584

c	18	611	56.1	619	9	AV911034	AV911034
	19	605.8	55.6	622	9	AV917406	AV917406
	20	604.4	55.5	639	9	AV934079	AV934079
	21	604	55.5	604	9	AV909802	AV909802
c	22	601.4	55.2	614	9	AV927987	AV927987
	23	582.4	53.5	599	9	AV942033	AV942033
c	24	569	52.2	597	9	AV935664	AV935664
	25	566.8	52.0	829	10	BE417937	BE417937
c	26	555.4	51.9	827	10	BF625164	BF625164
	27	559.2	51.3	578	9	AV936329	AV936329
c	28	557.4	51.2	591	9	AV912179	AV912179
	29	553	50.8	632	10	BF474988	BF474988
	30	551.8	50.7	556	9	AV932591	AV932591
c	31	546	50.1	667	10	BC904718	BC904718
	32	543.4	49.9	554	9	AV936963	AV936963
c	33	542	49.8	609	9	AV945334	AV945334
	34	537.4	49.3	548	9	AV935379	AV935379
c	35	537.4	49.3	580	9	AV924547	AV924547
	36	530.4	48.7	537	9	AV912284	AV912284
c	37	524.4	48.2	527	9	AV910104	AV910104
	38	521.4	47.9	538	9	AV910104	AV910104
	39	513.8	47.2	726	9	BE214463	BE214463
	40	508.8	46.7	646	10	BF952074	BF952074
	41	504.4	46.3	589	10	BF478600	BF478600
	42	502.4	45.8	546	9	AV941025	AV941025
	43	498.4	45.6	652	9	AV923428	AV923428
	44	497	45.1	814	10	BE417956	BE417956
	45	480.4	44.1	513	9	AV940721	AV940721

ALIGNMENTS

RESULT 1
LOCUS BF065877
DEFINITION HV_CEBD014D20f Hordeum vulgare seedling green leaf EST library
HVCNDA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
HV_CEBD014D20f, mRNA sequence.
ACCESSION BF065877.1 GI:10842516
VERSION EST.
KEYWORDS
SOURCE
ORGANISM Hordeum vulgare
barley.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae
; Triticeae; Hordeum.
REFERENCE
AUTHORS Wing,R., Close,T.J., Kleinof, A., Wise, R., Wei, F., Begum, D.,
Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi,
D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla) seedling
leaf cDNA library
Unpublished (2001)
CONTACT: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 653
Seq primer: AATTAACTCCTCACTAAGCG
High quality sequence stop: 758.
Location/Qualifiers
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/organism="Hordeum vulgare"
/cultivar="C116151 (Mla6)"
/db_xref="taxon:4513"
/clone="HV_CEBD014D20f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HVCNDA0005 (Blumeria challenged)"

/tissue_type="seedling green leaf"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
 C.I. 16151 (Ma6) Plants were greenhouse grown in the R
 wise lab at Iowa State University, Ames, IA; 7 day old
 green seedlings were challenged with isolate 5874 (AYRM16
) of Blumeria graminis f. sp. hordei, and leaves were
 harvested 20 and 24 hr post-inoculation and snap frozen;
 uninoculated leaves were harvested 20 hr post-inoculation
 (Wel, Wise). In the RJ Close lab at the University of
 California, Riverside, total RNA was prepared from each
 sample pool, equal quantities of all three RNA pools were
 combined, poly(A) RNA was purified from the mixture, one
 primary unamplified cDNA library was made, and 1 million
 pfu were in vivo excised to give pBluescript SK(-) cDNA
 phagemids (Choi, Close). Phagemids were plated and picked
 at the Clemson University Genomics Institute (CUGI) (Begum
 , Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
 , Rambo, Main). The sequence has been trimmed to remove
 vector sequence and contains a minimum of 100 bases of
 phred value 20 or above. For more details on library
 preparation and sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close RJ, Wing R, Kleinhoft A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (<http://wheat.pw.usda.gov/gsnpages/ggn/31/cover.html>)"

BASE COUNT 221 a 231 c 235 g 226 t
 ORIGIN

Query Match 75.8%; Score 825.4; DB 10; Length 913;
 Best Local Similarity 97.4%; Pred. No. 3.5e-157;
 Matches 860; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

QY 1 CTTCTAGGTCGTCGCGATGCGGCTCGGTGTGAGCGCCAGTACTGCGCCAGGTC 60
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 DB 33 CTTCTAGGTCGTCGCGATGCGGCTCGGTGTGAGCGCCAGTACTGCGCCAGGTC 92
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 QY 61 GACAGGGCGCGCGGCTTCGCGCTCATGCGCTCCAGGAGGAGCGCCCGCCATCATG 120
 |||||||
 DB 93 GACAGGGCGCGCGGCTTCGCGCTCATGCGCTCCAGGAGGAGCGCCCGCCATCATG 152
 |||||||
 QY 121 CTCGCGCTCGCATGCGATGCTGCGACCTATGATGTGAACAAGAACTGGTGTGCA 180
 |||||||
 DB 153 CTCGCGCTCGCATGCGATGCTGCGACCTATGATGTGAACAAGAACTGGTGTGCA 212
 |||||||
 QY 181 AATGCTTCAATTAGATGAGAGAGAGTACACCATGTTCAAAATGCTGCTTAAAAAT 240
 |||||||
 DB 213 AATGCTTCAATTAGATGAGAGAGAGTACACCATGTTCAAAATGCTGCTTAAAAAT 272
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 QY 241 GCTATTGATCTCTGAGCTATTAAAGGAGCATCAAGATTTCATATGAGACCTT 300
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 DB 273 GCTATTGATCTCTGAGCTATTAAAGGAGCATCAAGATTTCATATGAGACCTT 332
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 QY 301 CATCAGCTTGGCGAGTAGTTCAGTTGAAGTCACCGGGGGTCCCAACCGTTGAGTTTCA 360
 |||||||
 DB 333 CATCAGCTTGGCGAGTAGTTCAGTTGAAGTCACCGGGGGTCCCAACCGTTGAGTTTCA 392
 |||||||
 QY 361 CCTGGAAGACGATGTCGACGTTTCCCGGTAAGAGACGCTTCTGATGTTAAGAAA 420
 |||||||
 DB 393 CCTGGAAGACGATGTCGACGTTTCCCGGTAAGAGACGCTTCTGATGTTAAGAAA 452
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 QY 421 GSTGACCACTAAGGAGCATCTTTATCGAATGGGGTTAACAACAAAGATATTGTA 480
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 DB 453 GSTGACCACTAAGGAGCATCTTTATCGAATGGGGTTAACAACAAAGATATTGTA 512
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 QY 481 GCACATATCGGGGGACAGCGCTGGGAAGCGCATCTGAAGAGTCTGGGTTTGACGGT 540
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 DB 513 GCACATATCGGGGGACAGCGCTGGGAAGCGCATCTGAAGAGTCTGGGTTTGACGGT 572
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QY 541 GCATGACCTGTGACCCCTGTGAATTTGACACTCATCTTTCTTGAGTACTGAGGGG 600
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 DB 573 GCATGACCTGTGACCCCTGTGAATTTGACACTCATCTTTCTTGAGTACTGAGGGG 632
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 QY 601 GAATCTGAGGCTCTTGAGAGCTCCCTACGATGAAGCAATGTTGGATGATCTGTAATT 660
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 DB 633 GAATCTGAGGCTCTTGAGAGCTCCCTACGATGAAGCAATGTTGGATGATCTGTAATT 692
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 QY 661 CGACGATGTGAGCTTTATGCAAGAGATGAGATGTTTCTTCAAGAGTACCGTGA 720
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 DB 693 CGACGATGTGAGCTTTATGCAAGAGATGAGATGTTTCTTCAAGAGTACCGTGA 752
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 QY 721 TCACACAAAACTTTCTGTAACCTGCTTCACACAGAGAGAGTGGCCACATCTACA 780
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 DB 753 TCACACAAAACTTTCTGTAACCTGCTTCACACAGAGAGAGTGGCCACATCTACA 812
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 QY 781 AATATGATGTTTCACTGCTGTTTACCTGCACAGAGTCCAGTGGGTACAGTTGCT 840
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 DB 813 AATATGATGTTTCACTGCTGTTTACCTGCACAGAGTCCAGTGGGTACAGTTGCT 871
 |||||||
 QY 841 GCACCTGATGTTATCGCGGCTACTGTACGAGACTTCCACA 883
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 DB 872 GCAACTGTA-TTATTCGGGCTACCGGTCCAAAGTTCCAAAA 913
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RESULT 2
 BE705572/c 831 bp mRNA linear EST 12-SEP-2000
 LOCUS SC01.03b12.A SC01.AARC_ECORC_cold_stressed_winter_rye_seedlings
 DEFINITION Secale cereale cDNA clone SC01.03b12, mRNA sequence.
 ACCESSION BE705572
 VERSION BE705572.1 GI:10093837
 KEYWORDS rye.
 SOURCE
 ORGANISM

Secale cereale

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Secale.
 1 (bases 1 to 831)
 SINGH,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori
 J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
 Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
 Unpublished (2000)
 Contact: Singh,J.A.
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 960 Carling Avenue, Bldg. 20, Ottawa, Ontario, K1A 0C6, Canada
 Tel: (613) 759-1662
 Fax: (613) 759-1701
 Email: singhja@em.agr.ca.
 Location/Qualifiers

FEATURES

source
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 /organism="Secale cereale"
 /cultivar="Puma (winter rye)"
 /db_xref="taxon:4550"
 /clone="Sc01_03b12"
 /clone_1lb="Sc01.AARC_ECORC_cold_stressed_winter_rye_seedl
 ings"
 /tissue_type="leaf, crown"
 /dev_stage="seedling three-leaf stage"
 /note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI;
 Site_2: Xho I; Sampled three-leaf seedlings treated for
 one week at 20c, 12 hrs light/day. Library made with
 Stratagene UNIZAP XR Kit/GigaPack III Gold Kit. Lambda
 library is amplified, then mass excised in SOLR cells."

BASE COUNT 234 a 199 c 168 g 229 t 1 others
 ORIGIN

Query Match 64.3%; Score 700.6; DB 10; Length 831;
 Best Local Similarity 95.6%; Pred. No. 6.6e-137;
 Matches 752; Conservative 1; Mismatches 30; Indels 4; Gaps 3;

QY 288 AATATGAGACCTTCATCAGCTTGGCGAGTAGTTCAGATTGAAGTACACGGGGGTCCAAAC 347

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Db      831 ATATGAGACCTTATACCTGCTGAGATGATGAGTGAAGTCACC -GGGGGTCACAC 773
OY      348 CCTTGGATTCATCCCTGGAAGACGTGATTCGATGTTTGTCCCGTGAAGACGCTTCC 407
Db      772 CATTGAGTTCATCCCTGGAAGACGTGATTCATGATTTGCCCGTGAAGACGCTTCC 713
OY      408 TGATGCTAAGAAAGGTGACACACATCTAAGGACATCTTTATTCGANTGGGTTAAACA 467
Db      712 TGATGCTAAGAAAGGTGACACACATCTAAGGACATCTTTATTCGANTGGGTTAAACA 653
OY      468 CAAAGATATTTAGACATCTGAGGGGGACAGCCTGGGAAGGGGACATCCGAAAGGTC 527
Db      652 CAAAGATATTTAGACATCTGAGGGGGACAGCCTGGGAAGGGGACATCCGAAAGGTC 593
OY      528 TGGGTTTGGAGGTGACATGAGCTGACCCCTGAAATTTGACAACTCATCTTCTTGA 587
Db      592 TGGGTTTGGAGGTGACATGAGCTGACCCCTGAAATTTGACAACTCATCTTCTTGA 533
OY      588 GCTACTGAAGGGGGAATCTGAGGGTCTTGAAGCTCCCTACTGATTAAGGCAATGTGGA 647
Db      532 GCTACTGAAGGGGGAATCTGAGGGTCTTGAAGCTCCCTACTGATTAAGGCAATGTGGA 473
OY      648 TGATGCTAAGTTCGACGCTATGAGCTTATGCAAGGATGAGGATGTTTCTTCA 707
Db      472 TGATGCTAAGTTCGACGCTATGAGCTTATGCAAGGATGAGGATGTTTCTTCA 413
OY      708 GCACTACGCTGAATCACAACAAAATTTCTGAACTTGGCTTCAACACGAGGAGAGTGG 767
Db      412 GCACTACGCTGAATCACAACAAAATTTCTGAACTTGGCTTCAACACGAGGAGAGTGG 353
OY      768 CCCAGCATCTACAAAATCAGATGTTTCAACTGCTGTGACTTGAACAGAGTGCAGTGG 827
Db      352 CTCACATCTACAAAATCAGATGTTTCAACTGCTGTGACTTGAACAGAGTGCAGTGG 293
OY      828 GGTAGCAGTGTGAGCTGAGCTGATGCGGGGCTACCTGACGAAGCTTCCAAAGAGG 887
Db      292 GGTAGCAGTGTGAGCTGAGCTGATGCGGGGCTACCTGAGTGAAGGCTTCCAAAGAGG 233
OY      888 CAAAGTAAAGGGTTCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 947
Db      232 CAAAGTAAAGGGTTCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 173
OY      948 TATTTCAAAAATTAAGTCCCAAGTGCAAAATAACAACTGATGAGTGAACCAACA 1007
Db      172 TCTT-AAAAAATTAAGTCCCAAGTGCAAAATAACAACTGATGAGTGAACCAACA 114
OY      1008 GTAGTCTCAAAATTAATTCATACATCTTGAAGACATCTCCCTCATATATATCATATC 1067
Db      113 GCAGTCTTAAATTAATTCATACATCTTGAAGACATCTCCCTC--ATGATATCATCATAC 56
OY      1068 TTGAATA 1074
Db      55 TTGAATA 49

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RESULT 3
 AV936730/c 703 bp mRNA linear EST 18-JAN-2002
 LOCUS AV936730 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,
 DEFINITION heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
 clone baal5K17.3, mRNA sequence.
 ACCESSION AV936730
 VERSION AV936730
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare.
 ORGANISM Hordeum vulgare subsp. vulgare.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 703)
 AUTHORS Sato, K., Saitoh, D. and Takeda, K.
 TITLE Barley EST sequencing project in NIG and Okayama Univ

```

JOURNAL      Unpublished (2002)
COMMENT      Contact: Tadasu Shino-1
              Center For Genetic Resource Information
              National Institute of Genetics
              1111 Yata, Mishima, Shizuoka 411-8540, Japan
              Tel: 81-559-81-6856
              Fax: 81-559-81-6855
              Email: tshino@genes.nig.ac.jp.
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    /cultivar="Haruna Nijo"
    /db_xref="taxon:112509"
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    /clone_11b="K. Sato unpublished cDNA library, cv. Haruna
    Nijo adult, heading stage top three leaves".
    /tissue_type="top three leaves"
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    Query Match      62.3%; Score 678; DB 9; Length 703;
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    Matches 700; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
OY      364 GGAAGACGTGATTCGTCAGTGTGTCGCCGTGAAGACGCTTCTGATGCTAAGAAAGT 423
Db      703 GAAAGACGTGATTCGTCAGTGTGTCGCCGTGAAGACGCTTCTGATGCTAAGAAAGT 644
OY      424 GCACCAATCTAAGGACATCTTTATGATGAGGCTTACACACAAAGATTTGTAGCA 483
Db      643 GCACCAATCTAAGGACATCTTTATGATGAGGCTTACACAAAGATTTGTAGCA 584
OY      484 CTATCTGGGGGGCACAGCCTGGGAAAGGGGCAATCCGAAAGGCTGGGTTGACGGTGA 543
Db      583 CTATCTGGGGGGCACAGCCTGGGAAAGGGGCAATCCGAAAGGCTGGGTTGACGGTGA 524
OY      544 TGGACTCGTGACCTCTGAAATTTGACAACTCATCTTCTTGAAGCTGAAGGGGGA 603
Db      523 TGGACTCGTGACCTCTGAAATTTGACAACTCATCTTCTTGAAGCTGAAGGGGGA 464
OY      604 TCTGAGGGCTTCTGAGAGTCCCTACTGATTAAGGATGTTGATGATCTGAATTTGCA 663
Db      463 TCTGAGGGCTTCTGAGAGTCCCTACTGATTAAGGATGTTGATGATCTGAATTTGCA 404
OY      664 CGCTATGAGACCTTATGCAAGATGAGATGTTTCTTCAAGGACTAGCGTGAATCA 723
Db      403 CGCTATGAGACCTTATGCAAGATGAGATGTTTCTTCAAGGACTAGCGTGAATCA 344
OY      724 CACAAAACCTTCTGAACTTGGCTTCAACACGAGAGAGTGGCCAGCATCTACAAA 783
Db      343 CACAAAACCTTCTGAACTTGGCTTCAACACGAGAGAGTGGCCAGCATCTACAAA 284
OY      784 TCAGATGTTTCAACTGCTGTTGTACTTGACAGAGTGCAGTGGGGTGAAGTCTCTGA 843
Db      283 TCAGATGTTTCAACTGCTGTTGTACTTGACAGAGTGCAGTGGGGTGAAGTCTCTGA 224
OY      844 GCTGATTTATGCGGGGCTACCTGACGAGCTTCCAGAGGAGGCAAGTGAAGGGTGGT 903
Db      223 GCTGATTTATGCGGGGCTACCTGACGAGCTTCCAGAGGAGGCAAGTGAAGGGTGGT 164
OY      904 GAGTCTTGGATGACATTCCTTATTTAGTAATCAATCAATTTATTTAAAAATTA 963
Db      163 GAGTCTTGGATGACATTCCTTATTTAGTAATCAATCAATTTATTTAAAAATTA 104
OY      964 GTGCCAATGCAAAATTAACAGAACTAGTGAACCAACCAACATAGTCTCAAAATTT 1023
Db      103 GTGCCAATGCAAAATTAACAGAACTAGTGAACCAACCAACATAGTCTCAAAATTT 44
OY      1024 TCATACATT-CTTGAGAGCAT-CTCCTCATATATATACATCA 1064
Db      43 TCATACATTCTTGAGAGCATCTCCTCATATATATACATCA 1

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RESULT 4
LOCUS AV933174 674 bp mRNA linear EST 18-JAN-2002
DEFINITION AV933174 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baal5k17 5', mRNA sequence.

ACCESSION AV933174
VERSION AV933174.1 GI:18228971
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triliceae; Hordeum.
REFERENCE 1 (bases 1 to 674)
Sato, K., Saitoh, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
CONTACT: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
source 1..674
/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Haruna Nijo"
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/clone="baal5k17"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"
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/dev_stage="adult, heading stage"

BASE COUNT 159 a 165 c 187 g 163 t

ORIGIN
Query Match 61.7%; Score 671.4; DB 9; Length 674;
Best Local Similarity 99.9%; Pred. No. 5,4e-126;
Matches 672; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TAGGTCGTCGCCGATGCGGCTCGGCTGGAGACCCGACGATACCTGCGCCAGGTGAC 64
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DB 2 TAGGTCGTCGCCGATGCGGCTCGGCTGGAGACCCGACGATACCTGCGCCAGGTGAC 61
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QY 65 GGGCGCGCGGCGCTTCGCTGCGCTCATGCGCTCCAAAGGATGCGGCCCATCATGCTCG 124
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DB 62 GGGCGCGCGGCGCTTCGCTGCGCTCATGCGCTCCAAAGGATGCGGCCCATCATGCTCG 121
|||||
QY 125 GCGTCGATGCGATGCTGGCACCCTATGATGTGACACAAAGAACTGGTGTGAATG 184
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DB 122 GCGTCGATGCGATGCTGGCACCCTATGATGTGACACAAAGAACTGGTGTGAATG 181
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QY 185 GTTCAATTAGATAGAGAGAGATACACCATGTTCAATGCTGGCTTAAATTTGCTA 244
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DB 182 GTTCAATTAGATAGAGAGAGATACACCATGTTCAATGCTGGCTTAAATTTGCTA 241
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QY 245 TTGATCTCTTGAGCTATTAAAGGAACATCCAAAGATTGATATGAGACCTTCATC 304
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DB 242 TTGATCTCTTGAGCTATTAAAGGAACATCCAAAGATTGATATGAGACCTTCATC 301
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QY 305 AGCTTGCGGAGTAGTTGAGAGTGAAGTACCGGGGGTCCAAACCGTTGAGTTCATCC 364
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DB 302 AGCTTGCGGAGTAGTTGAGAGTGAAGTACCGGGGGTCCAAACCGTTGAGTTCATCC 361
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QY 365 GAAGAGCGATTCGTCAGATTTGTCCCGGGAAGAGACGCTTCCTGATGCTAAGAAAGTG 424
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DB 362 GAAGAGCGATTCGTCAGATTTGTCCCGGGAAGAGACGCTTCCTGATGCTAAGAAAGTG 421
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QY 425 CACCACTCTAAGGACATCTTTATGCAATGGGGTTAAGACAAAGATTTGTAGCAC 484
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DB 422 CACCACTCTAAGGACATCTTTATGCAATGGGGTTAAGACAAAGATTTGTAGCAC 481
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DB 482 TATCTGGGGGGGACAGCTGGGAAAGCGCATCTGAAAGGTCTGGGTTGACGGTGAT 541
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QY 545 GGAAGTGTGACCTCTGAAATTTGACAACTCATCTTTTGAAGTACTGAAGGGGAAT 604
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DB 542 GGAAGTGTGACCTCTGAAATTTGACAACTCATCTTTTGAAGTACTGAAGGGGAAT 601
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DB 602 CTGAGGCTCTTGAAGCTCCCTACTGATTAAGGCATGTGGATGATCCTGAATTTGAC 661
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DB 662 GCTATGTGAGCT 674
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RESULT 5
LOCUS AV927876/c 675 bp mRNA linear EST 18-JAN-2002
DEFINITION AV927876 K. Sato unpublished cDNA library, cv. Haruna Nijo second leaf stage seedling leaves Hordeum vulgare subsp. vulgare cDNA clone basd13b11 3', mRNA sequence.

ACCESSION AV927876
VERSION AV927876.1 GI:18223673
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triliceae; Hordeum.
REFERENCE 1 (bases 1 to 675)
Sato, K., Saitoh, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
CONTACT: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
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/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="basd13b11"
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/tissue_type="seedling leaves"
/dev_stage="second leaf stage"

BASE COUNT 187 a 156 c 135 g 196 t 1 others

ORIGIN
Query Match 61.0%; Score 664.4; DB 9; Length 675;
Best Local Similarity 99.7%; Pred. No. 1,4e-124;
Matches 665; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 675 TCCTGATGCTAAGAAAGTGACACCAATCAAGGACATCTTTATGCAATGGGTTAAC 616
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QY 465 AGCAAAAGATATTGACATCTATCTGGGGGACAGACGCTGGGAAGGGCATCTCGAAG 524
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DB 615 AGCAAAAGATATTGACATCTATCTGGGGGACAGACGCTGGGAAGGGCATCTCGAAG 556
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QY 525 GTCTGGGTTGACGGGTGATGATCTGATGACCTCTGAAATTTGACATCATACTTCT 584
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DB 555 GTCTGGGTTGACGGGTGATGATCTGATGACCTCTGAAATTTGACATCATACTTCT 496
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QY 585 TGAGCTACTGAAGGGGAATCTGAGGCTCTTGGAACTCCCTACTGATAGGCAATTGTT 644
 Db 495 TGAGCTACTGAAGGGGAATCTGAGGCTCTTGGAACTCCCTACTGATAGGCAATTGTT 436
 QY 645 GGATGATCTGAATTCGAGCGTATGAGCGCTTTTATGCAAGAGATGAGGATTTTCTT 704
 Db 435 GGATGATCTGAATTCGAGCGTATGAGCGCTTTTATGCAAGAGATGAGGATTTTCTT 376
 QY 705 CAAGAGCTAGCTGAATTCACACAAAAAATTTCTGAACCTTGCTGCACACAGGAGAG 764
 Db 375 CAAGAGCTAGCTGAATTCACACAAAAAATTTCTGAACCTTGCTGCACACAGGAGAG 316
 QY 765 TGGCCACGATCTACAAATACATGTTTAACTGCTGTGTACTTGACAGAGTCACT 824
 Db 315 TGGCCACGATCTACAAATACATGTTTAACTGCTGTGTACTTGACAGAGTCACT 256
 QY 825 CGGGGTAGAGCTGCTGACAGCTGATGATCGGGGCTACCTGAGCAAGCTTCAAGAG 884
 Db 255 CGGGGTAGAGCTGCTGACAGCTGATGATCGGGGCTACCTGAGCAAGCTTCAAGAG 196
 QY 885 GAGCAAGTAAAGGGGCTGCTGAGTCTTGGATGACATTCCTTATTTAGTAACTATCACT 944
 Db 195 GAGCAAGTAAAGGGGCTGCTGAGTCTTGGATGACATTCCTTATTTAGTAACTATCACT 136
 QY 945 TATTATTTCTAAAAAATTAAGTCCCAAGTGCATTAACAGAACTCTAGTGAACAACA 1004
 Db 135 TATTATTTCTAAAAAATTAAGTCCCAAGTGCATTAACAGAACTCTAGTGAACAACA 76
 QY 1005 ACGATGCTCAAAATATTTCATACATCTCTTGAGGACATCTCCTCATATATATATCA 1064
 Db 75 ACGATGCTCAAAATATTTCATACATCTCTTGAGGACATCTCCTCATATATATATCA 16
 QY 1065 TACTTGA 1071
 Db 15 TACTTGA 9
 RESULT 6
 AV945933/c 664 bp mRNA linear EST 18-JAN-2002
 LOCUS AV945933 K. Sato unpublished cDNA library, strain H602 adult.
 DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
 accession CDNA clone ban29a06 3', mRNA sequence.
 VERSION AV945933
 KEYWORDS AV945933.1 GI:18241730
 SOURCE EST.
 ORGANISM Hordeum vulgare subsp. spontaneum.
 Hordeum vulgare subsp. spontaneum.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 664)
 Sato, K., Saito, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ
 unpublished (2002)
 Contact: Tadao Shin-1
 Center for Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 Location/Qualifiers
 1. 664
 /organism="Hordeum vulgare subsp. spontaneum"
 /strain="H602"
 /db_xref="taxon:77009"
 /clone="ban29a06"
 /clone_lib="K. Sato unpublished cDNA library, strain H602
 adult, heading stage top three leaves"
 /tissue_type="top three leaves"
 /dev_stage="adult, heading stage"
 BASE COUNT 183 a 155 c 134 g 192 t

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 Best Local Similarity 100.0%; Pred. No. 1.7e-124;
 Matches 664; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 404 TTCTGATGCTAAGAAAGGTGACACACATATTAAGGACATCTTTATCGAATGGGTTAA 463
 Db 664 TTCTGATGCTAAGAAAGGTGACACACATATTAAGGACATCTTTATCGAATGGGTTAA 605
 QY 464 CAGACAAAGATATTGTAGCACTATTCGGGGGGGACAGACCCGGGAAAGGCGCATCTGAAA 523
 Db 604 CAGACAAAGATATTGTAGCACTATTCGGGGGGGACAGACCCGGGAAAGGCGCATCTGAAA 545
 QY 524 GGTCTGGGTTTGAAGGCTGACATGACATCGTACCCCTGTAATTTGACAACTCATCTTTC 583
 Db 544 GGTCTGGGTTTGAAGGCTGACATGACATCGTACCCCTGTAATTTGACAACTCATCTTTC 485
 QY 584 TTGAGCTACTGAAGGGGGAATCTGAGGCTCTTGAAGCTCCTACTGATTAAGCATTTGT 643
 Db 484 TTGAGCTACTGAAGGGGGAATCTGAGGCTCTTGAAGCTCCTACTGATTAAGCATTTGT 425
 QY 644 TTGATGATCTGAAATTTGACAGCTATTCGAGCTTATGCAAGTATGCAAGATGATTTTCT 703
 Db 424 TTGATGATCTGAAATTTGACAGCTATTCGAGCTTATGCAAGTATGCAAGATGATTTTCT 365
 QY 704 TCAAGGACTAGCTGATGATCACAACAAAAAATTTCTGAACTTGGCTTCACACAGGAGCA 763
 Db 364 TCAAGGACTAGCTGATGATCACAACAAAAAATTTCTGAACTTGGCTTCACACAGGAGCA 305
 QY 764 GTGGCCAGCATCTACAAATCAGATGTTTCAACTGCTGTGACTTGGACAGATGACAG 823
 Db 304 GTGGCCAGCATCTACAAATCAGATGTTTCAACTGCTGTGACTTGGACAGATGACAG 245
 QY 824 TCGGGGTAGAGCTTGGTGCAGCTGATGTTATCGCGGGCTACCTGTCGAAAGCTTCCAAGA 883
 Db 244 TCGGGGTAGAGCTTGGTGCAGCTGATGTTATCGCGGGCTACCTGTCGAAAGCTTCCAAGA 185
 QY 884 GGAGCAAGTAAAGGGGTTCTGAGTCTTGGATGACATTCCTTATTTAGTAACTATCAAG 943
 Db 184 GGAGCAAGTAAAGGGGTTCTGAGTCTTGGATGACATTCCTTATTTAGTAACTATCAAG 125
 QY 944 TTTTATTTCTAAAAAATTAAGTCCCAAGTGCATTAACAGAACTCTAGTGAACAACC 1003
 Db 124 TTTTATTTCTAAAAAATTAAGTCCCAAGTGCATTAACAGAACTCTAGTGAACAACC 65
 QY 1004 AACAGTAGTCAAAATATTTCATACATCTTGAGGACATCTCCTCATATATATATCATC 1063
 Db 64 AACAGTAGTCAAAATATTTCATACATCTTGAGGACATCTCCTCATATATATATCATC 5
 QY 1064 ATAC 1067
 Db 4 ATAC 1
 RESULT 7
 AV929644/c 662 bp mRNA linear EST 18-JAN-2002
 LOCUS AV929644 K. Sato unpublished cDNA library, cv. Haruna Nijo second
 DEFINITION leaf stage seedling leaves Hordeum vulgare subsp. vulgare cDNA
 accession AV929644
 VERSION AV929644.1 GI:18225441
 KEYWORDS EST.
 ORGANISM Hordeum vulgare subsp. vulgare.
 Hordeum vulgare subsp. vulgare.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 662)
 Sato, K., Saito, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ
 unpublished (2002)

COMMENT

Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES

source

1. 662
/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="basd14p20"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo second leaf stage seedling leaves"
/tissue_type="seedling leaves"
/dev_stage="second leaf stage"

BASE COUNT

183 a 155 c 133 g 191 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 662; DB 9; Length 662;
Pred. No. 4,3e-124;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 404 TTCCTATGCTAAGAAAGGTGCACACATCTAAGGACATCTTTATCGAATGGGGTTAA 463
DB 662 TTCCTATGCTAAGAAAGGTGCACACATCTAAGGACATCTTTATCGAATGGGGTTAA 603
OY 464 CAGACAAAGATATGTAGCTATCTGGGGGGGACACGCTGGGAAAGGGCATCTGTAA 523
DB 602 CAGACAAAGATATGTAGCTATCTGGGGGGGACACGCTGGGAAAGGGCATCTGTAA 543
OY 524 GGTCTGGGTTGACGGTGCATGACTCGTACCCTTGAATTTGACACTCATACTTTC 583
DB 542 GGTCTGGGTTGACGGTGCATGACTCGTACCCTTGAATTTGACACTCATACTTTC 483
OY 584 TTGAGCTACTGAAGGGGGAATCTGAGGGTCTTCTGAAGCTCCCTACTGATTAAGGCATTGT 643
DB 482 TTGAGCTACTGAAGGGGGAATCTGAGGGTCTTCTGAAGCTCCCTACTGATTAAGGCATTGT 423
OY 644 TGGATGATCTGAAATTTGACGCTATGTGAGGCTTTATGCAAGATGAGGATGTTTCT 703
DB 422 TGGATGATCTGAAATTTGACGCTATGTGAGGCTTTATGCAAGATGAGGATGTTTCT 363
OY 704 TCAAGGACTAGCGTGAATCACAACAAAACCTTCTGAACTTGGCTTCACACACGAGACA 763
DB 362 TCAAGGACTAGCGTGAATCACAACAAAACCTTCTGAACTTGGCTTCACACACGAGACA 303
OY 764 GTGGCCCAACATCTACAAAATCAGATGTTTCACTGCTGTTGTACTTGACACAGAGTCAG 823
DB 302 GTGGCCCAACATCTACAAAATCAGATGTTTCACTGCTGTTGTACTTGACACAGAGTCAG 243
OY 824 TGGGGGTAGCAGTTGCTGACGCTGTAGTTATCCGGGGCTACTGTACGAAAGCTTCCAGA 883
DB 242 TGGGGGTAGCAGTTGCTGACGCTGTAGTTATCCGGGGCTACTGTACGAAAGCTTCCAGA 183
OY 884 GGAGCAAGTAAGGGGTTCTGAGATCTTGGATGACATTCCTTATTTAGTAAGATACAG 943
DB 182 GGAGCAAGTAAGGGGTTCTGAGATCTTGGATGACATTCCTTATTTAGTAAGATACAG 123
OY 944 TTATTTATTTAAAAAATAGTCCCAAGTGCACAAATACAGACTCTAGTATGACAAAC 1003
DB 122 TTATTTATTTAAAAAATAGTCCCAAGTGCACAAATACAGACTCTAGTATGACAAAC 63
OY 1004 AACAGTAGTCTCAAAATATTTATCTATACATCTTGAGGACATCTCCTCATATATATACATC 1063
DB 62 AACAGTAGTCTCAAAATATTTATCTATACATCTTGAGGACATCTCCTCATATATATACATC 3
OY 1064 AT 1065
DB 2 AT 1

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RESULT 8

AV942984/c 662 bp mRNA linear EST 18-JAN-2002
LOCUS AV942984 K. Sato unpublished cDNA library, strain H602 adult.

DEFINITION

heading stage top three leaves Hordeum vulgare subsp. spontaneum
cDNA clone Dan15b23 3', mRNA sequence.

ACCESSION

AV942984
AV942984.1 GI:18238781

VERSION

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.

REFERENCE

1 (bases 1 to 662)
Sato, K., Saitoh, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
unpublished (2002)

JOURNAL

COMMENT

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Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES

source

1. 662
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"
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/clone="Dan15b23"
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/tissue_type="top three leaves"
/dev_stage="adult, heading stage" 1 others

BASE COUNT 180 a 155 c 134 g 192 t

ORIGIN

Query Match

Best Local Similarity 99.8%; Score 661; DB 9; Length 662;
Pred. No. 6,8e-124;
Matches 661; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 406 CTTGATGCTAAGAAAGGTGCACACATCTAAGGACATCTTTATCGAATGGGGTTAA 465
DB 662 CTTGATGCTAAGAAAGGTGCACACATCTAAGGACATCTTTATCGAATGGGGTTAA 603
OY 466 GACAAAGATTTGAGACTATCTGGGGGGGACACGCTGGGAAAGGGCATCTGTAAAG 525
DB 602 GACAAAGATTTGAGACTATCTGGGGGGGACACGCTGGGAAAGGGCATCTGTAAAG 543
OY 526 TCTGGGTTTACGCGTGCATGACCTGTAACCTCTGAAATTTGACAACTCATACTTCTT 585
DB 542 TCTGGGTTTACGCGTGCATGACCTGTAACCTCTGAAATTTGACAACTCATACTTCTT 483
OY 586 GACCTACTGAAGGGGGAATCTGAGGCTCTTGAAGCTCCCTACTGATTAAGGCATTGTG 645
DB 482 GACCTACTGAAGGGGGAATCTGAGGCTCTTGAAGCTCCCTACTGATTAAGGCATTGTG 423
OY 646 GATGATCCCTGAATTTGAGGCTATGTGAGGCTTTATGCAAGATGAGGATGTTTCTTC 705
DB 422 GATGATCCCTGAATTTGAGGCTATGTGAGGCTTTATGCAAGATGAGGATGTTTCTTC 363
OY 706 AAGGACTAGCGTGAATCACAACAAAACCTTCTGAACCTTGGCTTCACACAGGAGCAGT 765
DB 362 AAGGACTAGCGTGAATCACAACAAAACCTTCTGAACCTTGGCTTCACACAGGAGCAGT 303
OY 766 GGCCCAACATCTCAAAATACAGATGTTTCAACTGCTGTTGTAAGTGCACAGAGTCAGCT 825
DB 302 GGCCCAACATCTCAAAATACAGATGTTTCAACTGCTGTTGTAAGTGCACAGAGTCAGCT 243
OY 826 GGGGTAGCAGTTGCTGACGCTGTAGTTATCGGGGCTACTGTAAGGACTTCCAAAGAG 885
DB 242 GGGGTAGCAGTTGCTGACGCTGTAGTTATCGGGGCTACTGTAAGGACTTCCAAAGAG 183

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QY 886 AGCAAGTAAGGGGTCGTGAGTCTTGTGATGACATTCCTTATTTAGTAATCAAGTT 945
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DB 182 AGCAAGTAAGGGGTCGTGAGTCTTGTGATGACATTCCTTATTTAGTAATCAAGTT 123
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QY 946 ATTATTTCTAAAAAATTAAGTCCAGTAATACAGAACTCTAGTATGAACAACCA 1005
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DB 122 ATTATTTCTAAAAAATTAAGTCCAGTAATACAGAACTCTAGTATGAACAACCA 63
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QY 1006 CAGTACTCTCAAAATTAATTCATACATCTTGTGAGACATCTCCTTCATATATACATCAT 1065
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DB 62 CAGTACTCTCAAAATTAATTCATACATCTTGTGAGACATCTCCTTCATATATACATCAN 3
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QY 1066 AC 1067
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DB 2 AC 1

RESULT 9
AV937941 666 bp mRNA linear EST 18-JAN-2002
LOCUS AV937941 K. Sato unpublished cDNA library, strain H602 adult.
DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
CDNA clone ban15d3 5', mRNA sequence.
ACCESSION AV937941 GI:18233738
VERSION AV937941.1
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 666)
AUTHORS Sato, K., Saitoh, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
FEATURES
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/clone="ban15d3"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
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/dev_stage="adult, heading stage"
BASE COUNT 156 a 165 c 182 g 163 t
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Best Local Similarity 99.8%; Pred. No. 9,1e-124;
Matches 661; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTCTAGGTCGTCCGCGATGCGGCTCGGTGTGGAGCGCCAGTACCTGGCCAGGTC 60
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DB 5 CTTCTAGGTCGTCCGCGATGCGGCTCGGTGTGGAGCGCCAGTACCTGGCCAGGTC 64
    |||||||
QY 61 GACAGGGCGCGCGCGCTTCGTCGTCATCGCTCCCAAGGATGCGCCGCCATCAG 120
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DB 65 GACAGGGCGCGCGCGCTTCGTCGTCATCGCTCCCAAGGATGCGCCGCCATCAG 124
    |||||||
QY 121 CTCGCGCTGCATGCATGATCTGTGCACCTATGATGTGACACAAGAACTGATGTGCA 180
    |||||||
DB 125 CTCGCGCTGCATGCATGATCTGTGCACCTATGATGTGACACAAGAACTGATGTGCA 184
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QY 181 AATGTTCAATTAGATACGAGGAAGTACACCATGTTCAAAATGCTGCTTAAATTT 240
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DB 185 AATGTTCAATTAGATACGAGGAAGTACACCATGTTCAAAATGCTGCTTAAATTT 244
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QY 241 GCTATGATCTCTTTCAGGCTATTAAGGAAAGCATCCAAAGATTATCATATGACAGCTT 300
    |||||||
DB 245 GCTATGATCTCTTTCAGGCTATTAAGGAAAGCATCCAAAGATTATCATATGACAGCTT 304
    |||||||
QY 301 CATCAGCTTCCGCGAGTATTCAGTTGAAGTCACCGGGGTCACACGTTGATTCATC 360
    |||||||
DB 305 CATCAGCTTCCGCGAGTATTCAGTTGAAGTCACCGGGGTCACACGTTGATTCATC 364
    |||||||
QY 361 CCTGGAAGACGTGATTCGTCACTTGTGTCCTCCGTAAGGAGCGCTTCCTGATCTAAGAA 420
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DB 365 CCTGGAAGACGTGATTCGTCACTTGTGTCCTCCGTAAGGAGCGCTTCCTGATCTAAGAA 424
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QY 421 GGTGCACCATCTTAAGGAGCATCTTTTTCGAATGCGGTTTAACAGACAAATATGTA 480
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DB 425 GGTGCACCATCTTAAGGAGCATCTTTTTCGAATGCGGTTTAACAGACAAATATGTA 484
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QY 481 GCATATCTGGGGGGCAGACAGCTGGGAAAGCGCATCTGAAGAGTCTGGTTGACGCT 540
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DB 485 GCATATCTGGGGGGCAGACAGCTGGGAAAGCGCATCTGAAGAGTCTGGTTGACGCT 544
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DB 545 GCATGACTCTGACCCCTCTGAATTTGACAACTATACCTTTCTTGAGCTAGGAGGG 604
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QY 601 GAATCTGAGGCTCTTCTGAAGCTCCCTACTGATTAAGGCACTTTGTGATATCTGAATTT 660
    |||||||
DB 605 GAATCTGAGGCTCTTCTGAAGCTCCCTACTGATTAAGGCACTTTGTGATATCTGAATTT 664
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QY 661 CG 662
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DB 665 CG 666

RESULT 10
AV940735 677 bp mRNA linear EST 18-JAN-2002
LOCUS AV940735 K. Sato unpublished cDNA library, strain H602 adult.
DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
CDNA clone ban29a06 5', mRNA sequence.
ACCESSION AV940735 GI:18236532
VERSION AV940735.1
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 677)
AUTHORS Sato, K., Saitoh, D. and Takeda, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
FEATURES
source 1..677
/organism="Hordeum vulgare subsp. spontaneum"
/db_xref="taxon:77009"
/clone="ban29a06"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 158 a 169 c 185 g 165 t
ORIGIN

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Query Match 60.3%; Score 656.4; DB 9; Length 677;
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 Matches 657; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTCTAGGTCGTCGCGGATGAGGCGGCTCCGCTGTGACCGCATCTGCGCCAGCTC 60
 DB 20 CTTTATGAGGTCGTCGCGGATGAGGCGGCTCCGCTGTGACCGCATCTGCGCCAGCTC 79
 QY 61 GACAGGCGCGCGCGCGCTCCGCTGTGACCGCATCTGCGCCAGCTC 120
 DB 80 GACAGGCGCGCGCGCGCTCCGCTGTGACCGCATCTGCGCCAGCTC 139
 QY 121 CTCGCGCTGCGATGCGATGCTGCGCATATGATGTGAACACAGACTGTGTGCA 180
 DB 140 CTCGCGCTGCGATGCGATGCTGCGCATATGATGTGAACACAGACTGTGTGCA 199
 QY 181 AATGGTCAATTGATACGAGGAGATACACCATGCTTCAAAATGCTGCTTAAAT 240
 DB 200 AATGGTCAATTGATACGAGGAGATACACCATGCTTCAAAATGCTGCTTAAAT 259
 QY 241 GCTATGATCTCCTTGAAGCTATTAAGCAGACATCCAAAGATTACATATGACACCTT 300
 DB 260 GCTATGATCTCCTTGAAGCTATTAAGCAGACATCCAAAGATTACATATGACACCTT 319
 QY 301 CATCAGCTTGCAGGAGTGTGCAAGTGAACCGGGGGTCCAACTGTTGAGTTATC 360
 DB 320 CATCAGCTTGCAGGAGTGTGCAAGTGAACCGGGGGTCCAACTGTTGAGTTATC 379
 QY 361 CCGTGAAGACGATGATGCTGATGCTCCCGGAGGAGACGCTTCTGATGCTAAGAA 420
 DB 380 CCGTGAAGACGATGATGCTGATGCTCCCGGAGGAGACGCTTCTGATGCTAAGAA 439
 QY 421 GGTGACACCATCTAAGGAGCATCTTTATGATGAGGCTTAAACAGCAAAAGATATGTA 480
 DB 440 GGTGACACCATCTAAGGAGCATCTTTATGATGAGGCTTAAACAGCAAAAGATATGTA 499
 QY 481 GCACATCTTGGGGGGGACAGACCTGCGAAGGCGCATCTGAAAGTCTGGTTGACGT 540
 DB 500 GCACATCTTGGGGGGGACAGACCTGCGAAGGCGCATCTGAAAGTCTGGTTGACGT 559
 QY 541 GCATGAGTCTGAGGCTGCTGAAATTTGACAACTCACTTCTTGAAGTCAAGAGGG 600
 DB 560 GCATGAGTCTGAGGCTGCTGAAATTTGACAACTCACTTCTTGAAGTCAAGAGGG 619
 QY 601 GAATCTGAGGCTGCTTCTGAAAGTCTCTAGTATAGGAGCATCTTGTGATGATCTGAT 658
 DB 620 GAATCTGAGGCTGCTTCTGAAAGTCTCTAGTATAGGAGCATCTTGTGATGATCTGAT 677

RESULT 11
 LOCUS BF254606 863 bp mRNA linear EST 22-OCT-2001
 DEFINITION HVSMEF004H23f Hordeum vulgare seedling root EST library HVCNMA0007
 (Etiolated and unstressed) Hordeum vulgare cDNA clone
 HVSMEF004H23f, mRNA Sequence.

ACCESSION BF254606
 VERSION BF254606
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 863)
 WING, R., CLOSE, T.J., KLEINHOFS, A., WISE, R., BEGUM, D., FRISCH, D., YU
 , Y., HENRY, D., PALMER, M., RAMBO, T., SIMMONS, J., CHOI, D.W., FENTON
 , R.D., OATES, R. and MAIN, D.
 TITLE Development of a genetically and physically anchored EST resource
 for barley genomics: Morex unstressed seedling root cDNA library
 JOURNAL Unpublished (2001)
 COMMENT CONTACT: WING RA
 Clemson University Genomics Institute

Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 436
 Seq primer: AATTAACTCCTCACTAAAGGG
 High quality sequence start: 10
 High quality sequence stop: 787.
 Location/Qualifiers
 1. 863
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEF004H23f"
 /clone_lib="Hordeum vulgare seedling root EST library
 HVCNMA0007 (Etiolated and unstressed)"
 /issue_type="Seedling root"
 /lab_host="TUC121"
 /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
 Seeds were surface sterilized then germinated under aseptic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedling roots were
 then harvested, total RNA was prepared, poly(A) RNA was
 purified, one primary unamplified cDNA library was made,
 and 1 million pfu were in vivo excised to give plasmid
 SK(-) cDNA phagemids. These steps were performed in the TU
 close laboratory at the University of California,
 Riverside (Choi, Close, Fenton). Phagemids were plated and
 picked at the Clemson University Genomics Institute (CUGI)
 (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
 preparations, DNA sequencing and sequence analysis were
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
 , Rambo, Main). The sequence has been trimmed to remove
 vector sequence and contains a minimum of 100 bases of
 phred value 20 or above. For more details on library
 preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinhoofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html)"

BASE COUNT 212 a 231 g 209 t 1 others

Query Match 58.7%; Score 639.2; DB 10; Length 863;
 Best Local Similarity 89.7%; Pred. No. 1.8e-119;
 Matches 733; Conservative 0; Mismatches 74; Indels 10; Gaps 4;

QY 2 TTCTAGGTCGTCGCGGATGAGGCGGCTCCGCTGTGACCGCATCTGCGCCAGCTC 61
 DB 51 TTCTAGGTCGTCGCGGATGAGGCGGCTCCGCTGTGACCGCATCTGCGCCAGCTC 110
 QY 62 ACAGGCGCGCGCGCGCTCCGCTGTGACCGCATCTGCGCCAGCTC 121
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CDNA clone ba116f21 5', mRNA sequence.
ACCESSION AV938146
VERSION AV938146.1 GI:18233943
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SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 654)
AUTHORS Sato,K., Saitoh,D. and Takeda,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
FEATURES
source location/Qualifiers
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Best Local Similarity 99.8%; Pred. No. 4,2e-118;
Matches 633; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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LOCUS AV934694/c
DEFINITION AV934694 K. Sato unpublished cDNA library, cv. Hazuna Nijo adult,
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CDNA clone ba116f16 3', mRNA sequence.
ACCESSION AV934694
VERSION AV934694.1 GI:18230491
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 652)
AUTHORS Sato,K., Saitoh,D. and Takeda,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855

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RESULT 15
LOCUS AV909151 672 bp mRNA linear EST 18-JAN-2002
DEFINITION AV909151 K. Sato unpublished cDNA library, cv. Akashinriki
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baak1m21 5', mRNA sequence.
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VERSION AV909151.1 GI:18204700
KEYWORDS EST.
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ORGANISM Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 672)
Sato, K., Saitoh, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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Akashinriki vegetative stage leaves"
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/dev_stage="vegetative stage"
BASE COUNT 153 a 178 c 184 g 157 t
ORIGIN
Query Match 57.2%; Score 623.4; DB 9; Length 672;
Best Local Similarity 99.8%; Pred. No. 2.8e-116;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTTCTAGGGTCCTCCGCGATGGGGCTCGGTGTGGAGCGCGAGTACTGGCCAGGTC 60
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Db 48 CTTCTAGGGTCCTCCGCGATGGGGCTCGGTGTGGAGCGCGAGTACTGGCCAGGTC 107
QY 61 GACAGGGCGCGCGCGCTTCCTGCGCTCATCGCTCCCAAGGGATGCGCCCATCATG 120
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Db 108 GACAGGGCGCGCGCGCTTCCTGCGCTCATCGCTCCCAAGGGATGCGCCCATCATG 167
QY 121 CTCGCCCTCGCATGCGATGCTGCGACCTATGATGTGAACACAGAACTGGTGTGCA 180
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Db 168 CTCGCCCTCGCATGCGATGCTGCGACCTATGATGTGAACACAGAACTGGTGTGCA 227
QY 181 AATGGTTCAATTAGATACAGGAAGAGTACACCCATGGTTCAAACTGCTGCTTAAAAATT 240
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Db 228 AATGGTTCAATTAGATACAGGAAGAGTACACCCATGGTTCAAACTGCTGCTTAAAAATT 287
QY 241 GCTATTGATCTCCTTAGGCTATTAAAGCAAGCATCCAAAGATTACATATGACAGCTT 300
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Db 288 GCTATTGATCTCCTTAGGCTATTAAAGCAAGCATCCAAAGATTACATATGACAGCTT 347
QY 301 CATCAGCTTGCAGGAGTACTGTCAGTTGAAGTACCGGGGGTCCAAACGTTGAGTTCATC 360
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QY 361 CCGGAAGAGCGTATGCTGTCAGTTGTCCCGGAAGAGAGCGCTTCCATGCTAGAGAA 420
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Db 408 CCGGAAGAGCGTATGCTGTCAGTTGTCCCGGAAGAGAGCGCTTCCATGCTAGAGAA 467

QY 421 GGTCACACACATCTAAGGAGACATCTTTATCGAATGGGGTTAAACAGACAAAGATATTCTA 480
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Db 468 GGTGACACACATCTAAGGAGACATCTTTATCGAATGGGGTTAAACAGACAAAGATATTCTA 527
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Search completed: October 25, 2002, 17:29:25
Job time : 1727 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 16:18:41 ; Search time 50 Seconds

(without alignments)
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Title: US-09-870-501-2

Perfect score: 1089

Sequence: 1 cttcagggtcgtccgcgat.....gaataaaaaaaaaaaaaa 1089

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues 767066

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Issued_Patents.NA.*
- 2: /cgn2_6/ptodata/2/1na/5A.COMB.seq.*
- 3: /cgn2_6/ptodata/2/1na/5B.COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	174.2	16.0	557	1	US-08-266-451B-17
3	174.2	16.0	557	2	US-08-748-725-17
4	106.2	9.8	471	2	US-08-975-316-43
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6	37.8	3.5	1167	2	US-08-671-320-16
7	37.8	3.5	1167	2	US-08-868-577-16
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21	34.2	3.1	485	3	US-08-873-970-41
22	34.2	3.1	485	3	US-08-873-970-106
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24	34.2	3.1	485	4	US-09-095-855-106
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41	33.2	3.0	3498	3	US-09-421-868-1	Sequence 1, Appl
42	33.2	3.0	8920	2	US-08-446-855A-1	Sequence 1, Appl
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44	33.2	3.0	8920	2	US-08-107-676-26	Sequence 26, Appl
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ALIGNMENTS

RESULT 1
US-08-975-316-85
Sequence 85, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 1229 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-316-85
Query Match 27.9%; Score 303.6; DB 2; Length 1229;
Best Local Similarity 63.4%; Pred. No. 2.1e-83;
Matches 465; Conservative 0; Mismatches 269; Indels 0; Gaps 0;
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QY 496 CACAGCCTGGGAAAGCGCATCTGAAGAGTCTGGGTTTGACGGTGCATGAGCTGAC 555
Db 702 CACACCTTGGGAGATGACCAAGAGATCTGTTTGAAGAGACATGAGACCTCTAAC 761
QY 556 CCTGAAATTTGACAACTCATCTTCTGAGCTAGTGAAGGGGGAATCGAGGGCT 615
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RESULT 2

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US-08-266-451B-17
; Sequence 17, Application US/08266451B
; Patent No. 5623054
; GENERAL INFORMATION:
; APPLICANT: Zhang et al.
; TITLE OF INVENTION: CRUCIFER AFT PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,451B
; FILING DATE: 23-June-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Iech, Karen F.
; REGISTRATION NUMBER: 35,238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ. ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-266-451B-17

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Query Match 16.0%; Score 174.2; DB 1; Length 557;
Best local Similarity 68.5%; Pred. No. 8e-44;
Matches 261; Conservative 0; Mismatches 108; Indels 12; Gaps 1;

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RESULT 3

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US-08-748-725-17
; Sequence 17, Application US/08748725
; Patent No. 5859346
; GENERAL INFORMATION:
; APPLICANT: Zhang et al.
; TITLE OF INVENTION: CRUCIFER AFT PROTEINS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)

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SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,725
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/266,451
FILING DATE: 23-June-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/219002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 357
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-748-725-17
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Query Match 16.0%; Score 174.2; DB 2; Length 557;
Best Local Similarity 68.5%; Pred. No. 8e-44;
Matches 261; Conservative 0; Mismatches 108; Indels 12; Gaps 1;

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QY 514 CATCGTGAAGGTCTGGGTTGAGGTGACGTCGTCGACCGTCGTAATTTGACAAAC 573
DB 2 CACCCAGAGAGGTGAGGCTTTGATGAGACATGACCCAGAGCCGCTGAACTTGACAC 61
QY 574 TCATCTTCTTCTGACTACTGAGAGGGGAGTCTGAGGCTCTTCTGAAGCTCCCTACTGAT 633
DB 62 TCTTACTTCTGAGGAGTCTGTAAGAGAGATCAGAGGCTTTGAACTTCAACTGAC 121
QY 634 AAGCATTTGTTGAGATCTCTGATTTGAGCGCTATGTGAGCTTTTATGCAAGATGAG 693
DB 122 AAGACCTTATTTTGAAGACCCGAGATTCGCTCTGTTGAGCTTTATGCAAGATGAA 181
QY 694 GATGTTTCTTCAAGACGCTGATACACAAATGATGTTTCACTTGAACCTTGACCTGACA 753
DB 182 GATGATCTTTAGAGACTACGCGGAGATGACAAAGAACTCTGAGCTTGTTCAC 241
QY 754 CCAGCGAGAGTGGCCACATCTACAAATGATGATGTTTCACTGTTTACTTGA 813
DB 242 CCA-----AAGCTCTCAGACAGGCAAGACAGTTGCGAGACGATTTCTGCA 289
QY 814 CAGAGTGCAGTGGGGTACAGTGTCTGACAGCTGATGTTATCGGGGCTACTGTACGAA 873
DB 290 CAGAGTGGCTTGGGGTGGACAGTGTCTGCTGCGTGTGGCATTTTGTTTACGAG 349
QY 874 GCTTCCAGAGAGGAGCAAGTAA 894
DB 350 ATTGGAAGAGATGAAGTAA 370
```

RESULT 4

US-08-975-316-43
Sequence 43, Application US/08975316
Patent No. 5952486
GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVURKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA

```
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-316-43
```

Query Match 9.8%; Score 106.2; DB 2; Length 471;
Best Local Similarity 56.4%; Pred. No. 5.9e-23;
Matches 198; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

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QY 16 GCGATGGGGGCTCCGGTGTGGAGCCGCGTACCTGCGCCAGGTGACAGGGCGGCCGC 75
DB 103 GGGAGTCTTACCCAGCCTTAAGCCAGAGTACAAAGAGCTGTGAGAAATGCAAGAAG 162
QY 76 GCTTCCTGCTGCTCATGCTCCAAAGGATGCGCCCATCATCTCCGCTCGCATAG 135
DB 163 AAGTTGAGAGGCTCATGCTGAGAAAGCTCGCTCCGCTCATCTCCGCTCGCATAG 222
QY 136 CATGATGCTGCGACTATGATGTGAACACAGAACTGTGTGCAAAAGTTCATTTAGA 195
DB 223 CACTCGCGCGTACCTTGATGTGAAGACGAAGACCGGAGCGCTGCGGACATGAAG 282
QY 196 TACGAGGAAGATACACCATGCTCAATGCTGCTTAAATGCTATGATCTCTT 255
DB 283 CAGCGCGGAGCTCAAGCCAGGAGGACAGCGGAGCTGAGCTTGCAGATGAGTCTTG 342
QY 256 GAGCTATTAAAGCGAAGCATCAAAAGATTACATATGACAGACTTCATCAGCTTGC 315
DB 343 CAGCGATCAAGATCAGTATCCCGTCACTATGCTGATTTCTACAGAGCTGGCTGGC 402
QY 316 GTAGTTGACAGTGAAGTACCGGGGGTCCACCGTTGAGTATCATCCCTGGA 366
DB 403 GTCTGTGTGTGAAGTTACTGTGTGACCTGAAGTGTCTTTTACCCGGA 453
```

RESULT 5

US-07-929-580B-1/C
Sequence 1, Application US/07929580B
Patent No. 5426181
GENERAL INFORMATION:
APPLICANT: Lee, Tae Ho
APPLICANT: Lee, Gene W.
APPLICANT: Wilek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSC-14,
TITLE OF INVENTION: DNA Coding Therefor and Uses Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, NW
CITY: Washington

STATE: DC
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929,580B
FILING DATE: 19920814
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/640,492
FILING DATE: 14-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Guy Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: LEE25\VIJCEK-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1836 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 73..606
US-07-929-580B-1

Query Match 3.5%; Score 38; DB 1; Length 1836;
Best Local Similarity 55.2%; Pred. No. 0.14;
Matches 74; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 17 CGATGCGGGCTCCGGTGATGAGCGCCAGTACCTCGCCGCGCAGGTGACAGGGCGCGCGCG 76
Db 565 CGCGTGAGAGTGGCGGTGGCGCGCCGCTCTCAGCACCGCGGCGCGCGCGCGCGCG 506
QY 77 CCTCCGTCGCTCATCGCTCCAGAGGATGGCCCCCATCATGCTCCGCTCGCATGGC 136
Db 505 CCTCCTCTGGGGGCTGGCGCTCCGCGCCCTCATACGCGCACCGCTCGCGCGCGCTCGC 446
QY 137 ATGATCTGGCACC 150
Db 445 GGTGCGCTGCAGC 432

RESULT 6
US-08-671-320-16
Sequence 16, Application US/08671320
Patent No. 5840558
GENERAL INFORMATION:
APPLICANT: VIERLING JR, RICHARD A
TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1125 SO. 103RD STREET
STREET: SUITE 330
CITY: OMAHA
STATE: NE
COUNTRY: US
ZIP: 68124-1076
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/671,320
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JONDLE, ROBERT J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: 1227-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9000
TELEFAX: 402-398-9005
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..38
FEATURE:
NAME/KEY: CDS
LOCATION: 39..977
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 978..1167
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 39..101
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 102..977
US-08-671-320-16

Query Match 3.5%; Score 37.8; DB 2; Length 1167;
Best Local Similarity 66.7%; Pred. No. 0.12;
Matches 54; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 426 ACCACATCTAAGGAGACATCTTTATCGAATGGGCTTAACAGACAAGATATTGTAGCACT 485
Db 530 ATACACAACCTCGGCAAGACTTTTCTCAAGAGAGACTGTACGGGGAAGACTGTAGCTCT 589
QY 486 ATCTGGGGGGCACAGCCTGGG 506
Db 590 GTCCAGGGGGCACACTTTGGG 610

RESULT 7
US-08-868-577-16
Sequence 16, Application US/08868577
Patent No. 5866695
GENERAL INFORMATION:
APPLICANT: VIERLING JR, Richard A
TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kuiz
STREET: 555 13th Street NW, Suite 701 East
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,577
FILING DATE: 04-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:


```

NAME: Jondle, Robert J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1227-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-333-1550
TELEFAX: 402-333-1510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..38
FEATURE:
NAME/KEY: CDS
LOCATION: 39..977
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 978..1167
FEATURE:
NAME/KEY: sig.peptide
LOCATION: 39..101
FEATURE:
NAME/KEY: mat.peptide
LOCATION: 102..977
US-08-868-577-16

```

```

Query Match
Best Local Similarity 66.7%; Score 37.8; DB 2; Length 1167;
Matches 54; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

```

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QY 426 ACCACATCTAAGGACATCTTTATCGAATGGGTTACAGACAAATATGTAGCACT 485
DB 530 ATCACTACTGCGGCAAGACTTTTCTCAAGAGAGACTGTAGGGGAAGACTGTAGCTCT 589
QY 486 ATCTGGGGGGCACAGCCTGGG 506
DB 590 GTGAGGGGGGCACACTTGGG 610

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```

RESULT 8
US-08-753-007A-31/c
Sequence 31, Application US/08753007A
Patent No. 6074841
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,007A
FILING DATE: 19-NOV-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/699,591
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:

```

```

NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07334/022001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 2268 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 69...2009
OTHER INFORMATION:
US-08-753-007A-31

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Query Match
Best Local Similarity 55.6%; Score 36.4; DB 3; Length 2268;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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QY 11 GCTCCGCGATGGCGGCTCCGCTGCTGAGACGCCAGTACCTGGCCAGTCGACAGGCGCC 70
DB 1815 GCTCCGCGCTGCTCCGCTGCTGCTCCGACGCCAGGCTGAGCCGCCGCGCGCTCC 1756
QY 71 GCCGGGCTTCGCTCCGCTCCATCGCTCCAGAGATGCGCCGCCATCATGCTCCGCTCG 130
DB 1755 TCAGGAGACGAGTCCCTCCGCCGCCGCTGCGCGCCGCCAGCCGCTGAGAGCGCG 1696
QY 131 CATGCC 136
DB 1695 AGCGGC 1690

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RESULT 9
US-09-398-496-31/c
Sequence 31, Application US/09398496
Patent No. 6133423
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,496
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/753,007
FILING DATE: 19-NOV-1996
APPLICATION NUMBER: 08/699,591
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07334/022001
TELECOMMUNICATION INFORMATION:

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```

; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 69...2009
; OTHER INFORMATION:
; US-09-398-496-31

Query Match      3.3%  Score 36.4;  DB 3;  Length 2268;
Best Local Similarity 55.6%;  Pred No.0.49;
Matches 70;  Conservative 0;  Mismatches 56;  Indels 0;  Gaps 0;

QY  11  CGTCGCGATGCGCGGCTCCGTGAGACGCCGAGTACCTCGCCGACAGTCGACAGGCGGC 70
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   1815  CGTCGCGATGCGCGGCTCCGTGAGACGCCGAGTACCTCGCCGACAGTCGACAGGCGGC 1756

QY  71  GCGCGCGCTTCGCGTCCCTCATCGCTCCCAAGGATGCGCCGCCCATCATGCTCCGCTCG 130
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db   1755  TCACGCGACGAGTCCCTCGCGCCGCTGCGCGCTGCGCGCCGCGCCGCGTTCGAGGCGCG 1696

QY  131  CATGCG 136
      |||
Db   1695  AGCGCG 1690

RESULT 10
US-09-227-357-145
; Sequence 145, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08

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; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 145
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (79)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (138)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (144)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (625)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-227-357-145

Query Match      3.2%  Score 35;  DB 4;  Length 1048;
Best Local Similarity 55.3%;  Pred. No. 0.79;
Matches 68;  Conservative 0;  Mismatches 55;  Indels 0;  Gaps 0;

QY  967  CCAAGTGAATAATACAGAACTCTAGTGAATGAACAACCAAGTAGTCTCAAAATATTTC 1026

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Db      923 CCATTTTAAATAAGACCAAGAATTATTCTTAFAACCAACAGGTATGATAAATATGTC 982
        ||| |||| | ||| ||| ||||| ||| ||||| ||| ||||| |||
OY      1027 TACATCTTGAGGAATCTCCTTCATATATATACATCATACTTGATATAAAAAAAAAAAA 1086
        || | || | || | || | || | || | || | || | || | || | || |
Db      983 AATATCACTAATAACTGGGAAAATATCAAAATCAATCATAGTAAATAAAAAAAAAAAAA 1042
        || | || | || | || | || | || | || | || | || | || | || |
OY      1087 AAA 1089
        || |
Db      1043 AAA 1045

RESULT 11
       5198542-3/c
       Patent No. 5198542
       APPLICANT: ONDA, HARUO; ARIMURA, AKIRA; KIMURA, CHIHRU
       KITADA, CHEKO
       TITLE OF INVENTION: DNA ENCODING A PITUITARY ADENYLATE CYCLASE
       ACTIVATING PROTEIN AND USE THEREOF
       NUMBER OF SEQUENCES: 16
       CURRENT APPLICATION DATA:
       APPLICATION NUMBER: US/07/540,105
       FILING DATE: 10-JUN-1990
       SEQ ID NO.:3
       LENGTH: 1939
       5198542-3

```

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Query Match          3.2%; Score 34.8; DB 6; Length 1939;
Best Local Similarity 52.8%; Pred. No. 1.4;
Matches 75; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 925 TTATTTAGTAAATCAAGTATATATTTCTAAAAAATAAGTGCACAGTCAAAATAACAGA 984
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 890 TGATGTCTACTTTTCTATTTATTTTATTTAAAAACATAAACAGCTCGGGCAATTTTCA 831

QY 985 ACTCTAGTGTGAACCAACCAACAGTCTCAAAATATTTCATTAATCTTTAGGACATC 1044
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 830 TCTCTGTGCAGCGTTTGTATGAACCTCTCTATACCTTATATATATATATATATATA 771

QY 1045 TCTCTCATATATATATACATCAT 1066
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 770 TTCTTATATATATATTTATATAT 749

RESULT 12
US-08-076-011-1/c
: Sequence 1, Application US/08076011
: Patent No. 5521069
: GENERAL INFORMATION:
: APPLICANT: ONDA, Haruo
: APPLICANT: KIMURA, Chiharu
: APPLICANT: OHKUBO, Shoichi
: TITLE OF INVENTION: NOVEL DNA AND USE THEREOF
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN,
: ADDRESSEE: ROBERTS & CUSHMAN
: STREET: 130 Water Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: US
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/076.011
: FILING DATE: 11-JUN-1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/047,246

```

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1      FILING DATE: 13-APR-1993
2      NAME:
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: US 07/741,676
5      FILING DATE: 07-AUG-1991
6      NAME:
7      ATTORNEY/AGENT INFORMATION:
8      NAME: RESNICK, DAVID S
9      REGISTRATION NUMBER: 34235
10     REFERENCE/DOCKET NUMBER: 41155-CIP
11     TELECOMMUNICATION INFORMATION:
12     TELEPHONE: (617)523-3400
13     TELEFAX: (617)523-6440
14     TELEX: 200291 SPRE UR
15     INFORMATION FOR SEQ ID NO: 1:
16     SEQUENCE CHARACTERISTICS:
17     LENGTH: 17041 base pairs
18     TYPE: nucleic acid
19     STRANDEDNESS: double
20     TOPOLOGY: linear
21     MOLECULE TYPE: DNA (genomic)
22     FEATURE:
23     NAME/KEY: CDS
24     LOCATION: join(7540..7650, 9814..9945, 10421..10519)
25     LOCATION: 11602..11787)
26     OS-08-076-011-1

```

```

Query Match          3.2%: Score 34.8; DB 1, Length 17041;
Best Local Similarity 52.8%; Pred. No. 5.8;
Matches 75; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY   925  TTATTTACTAGTATCAAGTATTATTTCTTAATAAATAAGTGCCAAAGTCGAATTAACAGA 984
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   12149 TGATGTGCTACTTTTCTATTTATTTTTTATATAAACATTAACAGCTGGCGCATTTTCA 12090

QY   985  ACTGTAGTAGATGACAACCAACAGTAGTCTCAAAAATATTTCTATACATTTCTTGAGGACATC 1044
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   12089 TCCCTGTGCACAGCTTTGTATGAACCTCTCTATCTTATATATATATATATATATA 12030

QY   1045  TCCTTCATATATATATACATCAT 1066
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   12029 TTCTTATATATATATTTATATA 12008


RESULT 13
US-08-671-320-14
; Sequence 14, Application US/08671320
; Patent No. 5840558
; GENERAL INFORMATION:
; APPLICANT: VIERLING JR, RICHARD A
; TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
; TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 1125 SO. 103RD STREET
; STREET: SUITE 330
; CITY: OMAHA
; STATE: NE
; COUNTRY: US
; ZIP: 68124-1076
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671,320
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: JONDLIE, ROBERT J
; REGISTRATION NUMBER: 33,915
; REFERENCE/DOCKET NUMBER: 1227-001
```

```

? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 402-398-9000
? TELEFAX: 402-398-9005
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1191 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: 5'UTR
? LOCATION: 1..59
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 60..998
? FEATURE:
? NAME/KEY: 3'UTR
? LOCATION: 999..1191
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: 60..122
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 123..998
? OS-08-671-320-14 .

```

	Query Match	Score	DB 2:	length
Best Local Similarity	64.2%	Pred. No. 1.1'		
Matches	52:	Conservative	0:	Mismatches 29: Indels 0: Gaps 0:
OY	426	ACCAATATGAAGGACANCTTTATACGATGATGGGCTAACACACAAAGATATGTACACT	485	
Db	551	ATCACAACTGCGGCGCAAACTTCTCTCAGAAAGAGACTGTCAGGAGACCTGTGACTCT	610	
OY	486	ATCTGGGGGCGCACAGACTGGG	506	
Db	611	GTCAGGGGGGCGCACACTTTGGG	631	

RESULT 14
 US-08-868-577-14
 ; Sequence 14, Application US/08868577
 ; Patent No. 5868695
 ; GENERAL INFORMATION:
 ; APPLICANT: Vierling Jr., Richard A
 ; TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
 ; TITLE OF INVENTION: ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rothwell, Flagg, Ernst & Kurz
 ; STREET: 555 15th Street NW, Suite 701 East
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Wordperfect 6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/868,577
 ; FILING DATE: 04-JUN-1997
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jondle, Robert J.
 ; REGISTRATION NUMBER: 33,915
 ; REFERENCE/DOCKET NUMBER: N1227-003
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 402-333-1550
 ; TELEFAX: 402-333-1510
 ; INFORMATION FOR SEQ ID NO: 14:

```

? SEQUENCE CHARACTERISTICS:
LENGTH: 1191 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY : CDS
LOCATION : 60..998
FEATURE:
NAME/KEY : 5'UTR
LOCATION : 1..59
FEATURE:
NAME/KEY : 3'UTR
LOCATION : 999..1191
FEATURE:
NAME/KEY : sig_peptide
LOCATION : 60..122
FEATURE:
NAME/KEY : mat_peptide
LOCATION : 123..998
?-S-08-868--577-14
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	Query Match	3.2%	Score 34.6	DB 2	Length 1191
	Best Local Similarity	64.2%	Pred. No. 1.1		
	Matches	52	Conservative	0	Mismatches 29
					Indels 0
					Gaps 0
QY	426	ACCAACATCTAAGGAGAAATCTTTATCAAGTAATGGCGTTAACACAAACAATATTGTAGACAC	485		
DB	551	ATACACATCTCGGCCAAAGTTCTCTTAAAGAGAGACTGTACAGGGAGAACCTCGTAGCTCT	610		
QY	486	ATTGTGGGGGGCACAGCCTTGGG	506		
DB	611	GTCAGGGGGGGCACACCTTTGGG	631		

US-09-103-429A-1/c
Sequence 1, Application US/09103429A
Patent No. 6187558
GENERAL INFORMATION:
APPLICANT: Granados, Robert R
APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: CnA and Related Products and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Plinnist & Michaels, P.C.
STREET: 118 No. 6187558th Tlaga
CITY: Itasca
STATE: NY
COUNTRY: USA
ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,429A
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BTI-39
TELECOMMUNICATION INFORMATION:
TELEPHONE: (607) 256-3628
TELEFAX: (607) 256-3628
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2455 base pairs
TYPE: nucleic acid

```

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Trichoplusia ni
; TISSUE TYPE: peritrophic Membrane
; IMMEDIATE SOURCE:
; CLONE: IM14
; US-09-103-429A-1

```

```

Query Match          3.2%; Score 34.6; DB 4; Length 2455;
Best Local Similarity 55.4%; Pred. No. 1.8;
Matches 67; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

```

```

Qy 741 ACTTGCTTCACACACGAGCAGTGGCCACACATCTACAAATCAGATGTTCAACTGC 800
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 781 ATTGGGCAACAGTTCACAGATCGGGGCCAGACTGGGCTGAAGTGGGTGCAGAACACC 722
Qy 801 TGTGTACTTGCACAGAGTGCAGTGGGGGTAGCAGTTGCTGCAGCTGTAGTTATCGCGGG 860
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 721 TGGGGTACTTGCACGCGGGGTTGTCCGCCAGAGGGGTAGTTGCCGCCGGGGTACTTGCAGC 662
Qy 861 C 861
   |
Db 661 C 661

```

Search completed: October 25, 2002, 17:30:34
 Job time : 61 secs

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•
•
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:56:19 ; Search time 18 Seconds

(without alignments)
1553.444 Million cell updates/sec

Title: US-09-870-501-1

Perfect score: 1498
Sequence: 1 MAAPVDAEYLKQVDRARRA.....AVAAVYIAGLYEASRKS 291

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1240.5	82.8	288	2	T09845 L-ascorbate peroxi
2	1183	79.0	287	2	S71279 L-ascorbate peroxi
3	934.5	62.4	279	2	T04707 L-ascorbate peroxi
4	834.5	55.7	250	2	T07056 L-ascorbate peroxi
5	824.5	55.0	250	2	S68465 L-ascorbate peroxi
6	824.5	55.0	250	2	S49914 L-ascorbate peroxi
7	824	55.0	249	2	T10189 L-ascorbate peroxi
8	821.5	54.8	250	2	T03595 L-ascorbate peroxi
9	819.5	54.7	250	2	T09125 L-ascorbate peroxi
10	819.5	54.7	250	2	JF00232 L-ascorbate peroxi
11	818.5	54.6	250	2	D86214 L-ascorbate peroxi
12	818.5	54.6	263	2	S20866 L-ascorbate peroxi
13	815.5	53.6	250	2	S43157 L-ascorbate peroxi
14	802.5	53.6	250	2	A45116 L-ascorbate peroxi
15	775.5	51.8	260	2	T12389 L-ascorbate peroxi
16	774.5	51.7	245	2	T12334 L-ascorbate peroxi
17	752.5	50.2	250	2	T08071 L-ascorbate peroxi
18	746.5	49.8	254	2	T12338 L-ascorbate peroxi
19	714.5	47.8	309	2	S66265 L-ascorbate peroxi
20	666	44.5	421	2	S71331 L-ascorbate peroxi
21	653	43.6	430	2	T12282 L-ascorbate peroxi
22	644.5	43.0	421	2	T10190 L-ascorbate peroxi
23	640.5	42.8	426	2	C96804 L-ascorbate peroxi
24	631.5	42.2	372	2	T14193 L-ascorbate peroxi
25	598	39.9	327	2	T08103 L-ascorbate peroxi
26	457	30.5	361	1	OPBYC cytochrome-c perox
27	317	21.2	735	1	J50520 catalase (EC 1.11.
28	317	21.2	751	4	T43873 catalase (EC 1.11.
29	317	21.2	751	4	T43874 catalase (EC 1.11.

30	317	21.2	751	4	T43878 catalase (EC 1.11.
31	317	21.2	751	4	T43880 catalase (EC 1.11.
32	317	21.2	751	4	T43881 catalase (EC 1.11.
33	317	21.2	752	4	T43877 catalase (EC 1.11.
34	317	21.2	753	4	T43882 catalase (EC 1.11.
35	309.5	20.7	735	2	B83763 catalase BH0906 (I
36	294.5	19.7	724	2	B82186 catalase/peroxidase
37	294	19.6	737	2	AC0403 catalase (EC 1.11.
38	289.5	19.3	723	2	AF3127 catalase (imported
39	289.5	19.3	731	2	C98160 catalase (AB033631
40	280.5	18.7	731	2	T44846 catalase (EC 1.11.
41	277	18.5	736	2	T00313 catalase (EC 1.11.
42	276.5	18.5	736	2	T44562 catalase (EC 1.11.
43	266	17.8	754	2	S75113 catalase (EC 1.11.
44	265	17.7	741	2	A69529 catalase (EC 1.11.
45	261	17.4	166	2	T05342 L-ascorbate peroxi

ALIGNMENTS

```
RESULT 1
T09845
L-ascorbate peroxidase (EC 1.11.1.11), glyoxysomal - upland cotton
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Apr-2000
C:Accession: T09845
R:Bunkelmann, J.; Trelease, R.N.
submitted to the EMBL Data Library, September 1995
A:Description: Ascorbate peroxidase: A prominent membrane protein in oilseed glyoxyso
A:Reference number: Z16882
A:Accession: T09845
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-288 <BUN>
A:Cross-references: EMBL:U37060; NID:g1019945; P1D:g1019946
A:Experimental source: cultivar Deltapine 62
C:Function:
A:Description: catalyzes peroxidation of ascorbate to dehydroascorbate
C:Superfamily: cytochrome-c peroxidase
C:Keywords: chromoprotein; glyoxysome; heme; iron; metalloprotein; oxidoreductase
F:40/Active site: His (distal axial ligand) #status predicted
F:160/Binding site: Heme iron (His) (proximal axial ligand) #status predicted
F:176,205/Active site: Tyr, Asp #status predicted

Query Match      82.8%  Score 1240.5:  DB 2:  Length 288;
Best local similarity 80.4%:  Pred. No. 3e-95;  Mismatches 26;  Indels 3;  Gaps 1;
Matches 234;  Conservative

OY  1  MAAPVDAEYLKQVDRARRAPRALIASKGAPIMRLAMHMDAGTYDVNTRTGGANGSIRY  60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  1  MAFPVDEYLEIKEDIKARDRLALIALKNCAPIMLRLAMHMDAGTYDVSKTGGPGRSIRN  60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY  61  EEEYHGSNAGIKIAIDLEPKAKHPKITTYADLHQLAGVAAYEVYGGPVEFFIGRDS  120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  61  EEEFHHGANSGLIKIADICEEYKAKHPKITTYADLQLGVAAYEVYGGPTIDFVYGRKDS  120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY  121  SVCPEGRRLPDKKGAPHLRDFYRNGLTDRDITVALSGHSIGKAPRPSGDDGAWTRDP  180
    ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
DB  121  NICEPEGRLPDKKRAKAPHLRDFYRNGLSDDKIDVALSGHTLGRAPRPSGDDGFWTRDP  180
    ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||

OY  181  LKFDNSYFLELLKGSSEGLIKLPTDKALLDDPEFRYYVELYAKDDEVFKEKYDAESHKRLS  240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  181  LKFDNSYFLELLKGSSEGLIKLPTDKALLDDPEFRKYVELYAKDDEDAFPRDYAESHKRLS  240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY  241  ELGFPFRSSGPASTSDYSTAVNVAQAQSAVGVAVAAYVYIAGLYEASRKS  291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB  241  ELGFPFRS---ARSKVMWKSDTVIAQAGAVAAVAAYVILSYFEVRRMK  288
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
S71279
L-ascorbate peroxidase (EC 1.11.1.11) - Arabidopsis thaliana
```

N:Alternate names: protein M4E13.60
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
 C:Accession: S71279; T05770
 R:Jepsen, H.M.; Kirsgaard, I.V.H.; Melander, K.G.
 submitted to the EMBL Data Library, May 1996
 A:Description: Ascorbate peroxidase isoenzymes in Arabidopsis thaliana.
 A:Reference number: S71279
 A:Accession: S71279
 A:Molecule type: mRNA
 A:Residues: 1-287 <JES>
 A:Cross-references: EMBL:X98003; NID:g1332438; PID:g1332439
 R:Bevan, M.; Purnelle, B.; Boutry, M.; Goffeau, A.; Hohelsel, J.; Mewes, H.W.; Mayer, K.
 submitted to the Protein Sequence Database, April 1998
 A:Reference number: Z15451
 A:Accession: T05770
 A:Molecule type: DNA
 A:Residues: 1-287 <BEV>
 A:Cross-references: EMBL:AL022023
 A:Experimental source: cultivar Columbia; BAC clone M4E13
 C:Genetics:
 A:Gene: APX
 A:Map position: 4
 A:Introns: 38/2; 80/1; 96/3; 118/3; 135/1; 162/3; 189/2; 223/3
 A:Note: M4E13.60
 C:Superfamily: cytochrome-c peroxidase
 C:Keywords: heme; iron; metalloprotein; oxidoreductase
 F:40/Active site: His (distal axial ligand) #status predicted
 F:160/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 F:176,205/Active site: Trp, Asp #status predicted

Query Match 79.0%; Score 1183; DB 2; Length 287;
 Best local Similarity 75.9%; Pred. No. 1.7e-90;
 Matches 221; Conservative 34; Mismatches 32; Indels 4; Gaps 1;

QY 1 MAAPVDAEYLROVDARARAFRALIASKGAPIMLRAMHDAGTYDNTRTGANGSIRYEE 60
 DB 1 MAAPVDAEYLKEITKARDELRLINKNCAPIMLRAMHDAGTYDAOSTGTGGPNSIRN 60
 QY 61 EEEYTHGNSAGLKIADLLEPIKAKHPKITTYADLHQLAGVAAVETGGPTVEEIPGRDS 120
 DB 61 EEEHTHGANSGLKIALDLCEGVAKHPKITTYADLYQLAGVAAVEVGGPDIVFPGRKDS 120
 QY 121 SVCPREGRLPDAKKAPHLRDIYRMGLTDKDIVALSGSHLSKAHPERGFGPAWTRDP 180
 DB 121 NVCPREGRLPDAKQGFQRLRDYERNGLSDDKDIVALSGGTTLRAPHERSGFGPWPQEP 180
 QY 181 LKFDNSYFLELKGESGGLKLPDALKALDDPEFRRYVELYAKDEVFEDVESHKRLS 240
 DB 181 LKFDNSYFLELKGESGGLKLPDALKALDDPEFRRLVELYAKDEDAFFDYESHKRLS 240
 QY 241 ELGFPTRSSGPASTRKSDVSTAVVLAQSAVGAVAVAAVIAGTYLEASKRSK 291
 DB 241 ELGFNPNSAGKA---VADSTILAQSAFCVAAVAAVAFGYEYTRKRKK 287

RESULT 3
 T04707
 L-ascorbate peroxidase (EC 1.11.1.11) T19K4.100 - Arabidopsis thaliana
 N:Alternate names: protein F4B14.240
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-Apr-2000
 C:Accession: T04707; T05489
 R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, October 1998
 A:Reference number: Z15380
 A:Accession: T04707
 A:Molecule type: DNA
 A:Residues: 1-279 <BEV>
 A:Cross-references: EMBL:AL031986
 A:Experimental source: cultivar Columbia; BAC clone F4B14
 R:Bevan, M.; Wodler, H.; Wambutt, R.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X.; Schwellbe
 submitted to the Protein Sequence Database, April 1998

A:Reference number: Z15418
 A:Accession: T05489
 A:Molecule type: DNA
 A:Residues: 1-279 <BEV>
 A:Cross-references: EMBL:AL022373
 A:Experimental source: cultivar Columbia; BAC clone T19K4
 C:Genetics:
 A:Map position: 4
 A:Introns: 37/2; 79/1; 95/3; 117/3; 133/1; 160/3; 187/2; 221/3
 A:Note: F4B14.240; T19K4.100
 C:Superfamily: cytochrome-c peroxidase
 C:Keywords: heme; iron; metalloprotein; oxidoreductase
 F:39/Active site: His (distal axial ligand) #status predicted
 F:158/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 F:174,203/Active site: Trp, Asp #status predicted

Query Match 62.4%; Score 934.5; DB 2; Length 279;
 Best local Similarity 62.6%; Pred. No. 6.5e-70;
 Matches 179; Conservative 42; Mismatches 54; Indels 11; Gaps 2;

QY 6 VDAEYLROVDARARAFRALIASKGAPIMLRAMHDAGTYDNTRTGANGSIRYEE 65
 DB 5 VDAEYLKEITKTRDRLALISSRNCAPIMLRAMHDAGTYDAKKKTGANGSIRFEELN 64
 QY 66 HGSNAGLKIADLLEPIKAKHPKITTYADLHQLAGVAAVETGGPTVEEIPGRDSVCP 125
 DB 65 RPHNKGLEKAVAPCEYKAKHPKITSYADLYQLAGVAAVETGGPALPFPGRKDSAD- 123
 QY 126 EGRLPDAKKAPHLRDIYRMGLTDIYALSGSHLSKAHPERGFGPAWTRDPKRDN 185
 DB 124 DGLPDPNDEGASHLRTLFSSMGLDDIYALSGSHLGAHHERSDPEGPWTQDLPKFDN 183
 QY 186 SYFLELKGESGGLKLPDALKALDDPEFRRYVELYAKDEVFEDVESHKRLSELGPT 245
 DB 184 SYFVELKGETPELQDKTDKALDDPKFHPFVKLYAKDEDFPFAVATSHKRLSELGPN 243
 QY 246 PRSSGPASTRKSDVSTAVVLAQSAVGAVAVAAVIAGTYLEASKRSK 291
 DB 244 PPRRIPSA-----VTQYTLGIAVAAVAVITFYCEASRRK 279

RESULT 4
 T07056
 L-ascorbate peroxidase (EC 1.11.1.11) 2 - soybean
 C:Species: Glycine max (soybean)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 19-May-2000
 C:Accession: T07056
 R:Turano, F.J.; McMahon, M.B.; Caldwell, C.R.
 submitted to the EMBL Data Library, April 1996
 A:Reference number: Z15888
 A:Accession: T07056
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-250 <TUR>
 A:Cross-references: EMBL:U56634; NID:g1336081; PIDN:AA01221.1; PID:g1336082
 A:Experimental source: cv. Century
 C:Genetics:
 A:Gene: APX2
 A:Function:
 A:Description: catalyzes peroxidation of ascorbate to dehydroascorbate
 C:Superfamily: cytochrome-c peroxidase
 C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
 F:42/Active site: His (distal axial ligand) #status predicted
 F:163/Binding site: heme iron (His) (proximal axial ligand) #status predicted
 F:179,208/Active site: Trp, Asp #status predicted

Query Match 55.7%; Score 834.5; DB 2; Length 250;
 Best local Similarity 65.3%; Pred. No. 1.1e-61;
 Matches 158; Conservative 32; Mismatches 51; Indels 1; Gaps 1;

QY 4 PVDAEYLROVDARARAFRALIASKGAPIMLRAMHDAGTYDNTRTGANGSIRYEE 63
 DB 6 PTVSADYQKAVEAKKKLKGFTIAKRCAPIMLRAMHSAGYDVSSKGTGGPTGIKHPSE 65

Query Match 55.0%; Score 824; DB 2; Length 249;
Best Local Similarity 64.3%; Pred. No. 8.1e-61;
Matches 155; Conservative 32; Mismatches 54; Indels 0; Gaps 0;

QY 4 PYYDAEYLROVDRARRAFALITASKGAPIMLRAMHAGTYDVNTRTGANGSIRYEE 63
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 6 PVSSEYQKAIERAKKRLKGLTAERKCAPMLRLAMHSGTFCDSKGTGPFETMRKSE 65
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 64 YTHGSNAGLKIAIDLEPIKAKHPKITTYADLHQLAGVVAEVTGPTVEFIPGRDSSVC 123
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 66 LAHGANGGLDIIVRLLEPIKEGFPEITVADFYQLAGVVAEVTGPDVPHREDKREP 125
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 124 PREGRLPDAKKAPPHLRDIFRMRGLTDKDIYALSGHSLGKAPERSGFGDANTRDPLK 183
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 126 PREGRLPDATKGSDDLROVFTYMGSLSDODIYALSGHSLGKAPERSGFGDANTRDPLK 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 184 DMSYFLELLKGSEGLIKPTDKALLDDPEFRRYVELYAKDEVPFKDAESHKKTSEL 243
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 186 DSYTELLTGKESGILLQLASDKALLSDPVFRPLVERKYADDAFADYAEAHOKLSEL 245
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 244 F 244
|
DB 246 F 246

RESULT 8
T03595
L-ascorbate peroxidase (EC 1.11.1.11) [validated] - rice
N:Alternate names: 27K protein 4302; acetolactate synthetase I [misidentification]
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 20-Jun-2000
R:Accession: T03595; PS0211; PA0113; PQ0736
R:Morita, S.; Kaminaka, H.; Yokoi, H.; Masumura, T.; Tanaka, K.
A:Description: Cloning and characterization of a rice ascorbate peroxidase cDNA.
A:Reference number: 214966
A:Accession: T03595
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-250 <MOR>
A:Cross-references: EMBL:D45423
R:Tsuigita, A.; Kamo, M.
submitted to JIPID, April 1993
A:Reference number: PS0209
A:Accession: PS0211
A:Molecule type: protein
A:Residues: 2-17, 'X', 19 <TSU>
A:Experimental source: seed and callus (strain Nihonbare)
A:Note: molecular weight 27K, pI 5.5
R:Kamo, M.; Tsuigita, A.
submitted to JIPID, March 1995
A:Reference number: PA0114
A:Accession: PA0113
A:Molecule type: protein
A:Residues: 2-17, 'X', 19 <KAM>
A:Experimental source: seedling and callus
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A:Reference number: PQ0696
A:Accession: PQ0736
A:Status: preliminary
A:Molecule type: protein
A:Residues: 2, 'L', 4-19 <KOM>
C:Superfamily: cytochrome-c peroxidase
C:Keywords: heme; iron; metalloprotein; oxidoreductase
F:42/Active site: His (distal axial ligand) #status predicted
F:163/Binding site: heme iron (His) (proximal axial ligand) #status predicted
F:179,208/Active site: Trp, Asp #status predicted

Query Match 54.8%; Score 821.5; DB 2; Length 250;
Best Local Similarity 64.5%; Pred. No. 1.3e-60;

Matches 156; Conservative 34; Mismatches 51; Indels 1; Gaps 1;

QY 4 PYYDAEYLROVDRARRAFALITASKGAPIMLRAMHAGTYDVNTRTGANGSIRYEE 63
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 6 PVSSEYQKAIERAKKRLKGLTAERKCAPMLRLAMHSGTFCDSKGTGPFETMRKSE 65
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 64 YTHGSNAGLKIAIDLEPIKAKHPKITTYADLHQLAGVVAEVTGPTVEFIPGRDSSVC 123
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 66 LSHANAGGLDIIVRLLEPIKEGFPEITVADFYQLAGVVAEVTGPDVPHREDKREP 125
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 124 PREGRLPDAKKAPPHLRDIFRMRGLTDKDIYALSGHSLGKAPERSGFGDANTRDPLK 182
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 126 PREGRLPDATKGSDDLROVFTYMGSLSDODIYALSGHSLGKAPERSGFGDANTRDPLK 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 183 FDNYSFLELLKGSEGLIKPTDKALLDDPEFRRYVELYAKDEVPFKDAESHKKTSEL 242
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 186 FDNYSFLELLSGKESGLLQPSDKALLSDPARPLVERKYADDAFADYAEAHOKLSEL 245
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 243 GF 244
|
DB 246 GF 247

RESULT 9
T09125
L-ascorbate peroxidase (EC 1.11.1.11) - spinach
C:Species: Spinacia oleracea (spinach)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
R:Accession: T09125
R:Webb, R.P.; Allen, R.D.
Plant Physiol. 108, 1325, 1995
A:Title: Isolation and characterization of a cDNA for spinach cytosolic ascorbate per
A:Reference number: 216576; MUID:95357433
A:Accession: T09125
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-250 <WEB>
A:Cross-references: EMBL:L20864; NID:g310586; PIDN:AAA9518.1; PID:g310587
A:Experimental source: leaf
C:Function:
A:Description: catalyzes peroxidation of ascorbate to dehydroascorbate
C:Superfamily: cytochrome-c peroxidase
C:Keywords: chromoprotein; cytosol; heme; iron; metalloprotein; oxidoreductase
F:42/Active site: His (distal axial ligand) #status predicted
F:163/Binding site: heme iron (His) (proximal axial ligand) #status predicted
F:179,208/Active site: Trp, Asp #status predicted

Query Match 54.7%; Score 819.5; DB 2; Length 250;
Best Local Similarity 64.0%; Pred. No. 1.9e-60;
Matches 155; Conservative 31; Mismatches 55; Indels 1; Gaps 1;

QY 4 PYYDAEYLROVDRARRAFALITASKGAPIMLRAMHAGTYDVNTRTGANGSIRYEE 63
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 6 PVSSEYQKAIERAKKRLKGLTAERKCAPMLRLAMHSGTFCDSKGTGPFETMRKSE 65
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 64 YTHGSNAGLKIAIDLEPIKAKHPKITTYADLHQLAGVVAEVTGPTVEFIPGRDSSVC 123
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 66 LAHGANGGLDIIVRLLEPIKEGFPEITVADFYQLAGVVAEVTGPDVPHREDKREP 125
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 124 PREGRLPDAKKAPPHLRDIFRMRGLTDKDIYALSGHSLGKAPERSGFGDANTRDPLK 182
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 126 PREGRLPDATKGSDDLROVFTYMGSLSDODIYALSGHSLGKAPERSGFGDANTRDPLK 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 183 FDNYSFLELLKGSEGLIKPTDKALLDDPEFRRYVELYAKDEVPFKDAESHKKTSEL 242
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
DB 186 FDNYSFLELLSGKESGLLQPSDKALLSDPVFRPLVERKYADDAFADYAEAHOKLSEL 245
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |
QY 243 GF 244
|
DB 246 GF 247

RESULT 10

JE0232
L-ascorbate peroxidase (EC 1.11.1.11) - garden strawberry
N:Alternate names: APX
C:Species: Fragaria x ananassa (garden strawberry)
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-May-2000
C:Accession: JE0232
R:Kim, I.J.; Chung, W.I.
B:BioSci. Biotechnol. Biochem. 62, 1358-1363, 1998
A:Title: Isolation of genomic DNA containing a cytosolic ascorbate peroxidase gene (APX)
A:Reference number: JE0232; MUID:98386687
A:Accession: JE0232
A:Molecule type: DNA
A:Residues: 1-250 <KIN>
A:Cross-references: GB:AF039953; NID:92754859; PIDN:AB95222.1; PID:92754860
C:Genetics:
A:Gene: APXSC
A:Introns: 40/2 98/3 120/3 137/1 165/3 192/2 226/3 246/2
C:Superfamily: cytochrome-c peroxidase
C:Keywords: heme; iron; metalloprotein; oxidoreductase
F:42/Active site: His (distal axial ligand) #status predicted
F:163/Binding site: heme iron (His) (proximal axial ligand) #status predicted
F:179,208/Active site: Trp, Asp #status predicted

Query Match 54.7%; Score 819.5; DB 2; Length 250;
Best Local Similarity 64.9%; Pred. No. 1.9e-60;
Matches 157; Conservative 29; Mismatches 55; Indels 1; Gaps 1;

4 PVVDAEYLROVDARRARALIASKCAPIMRLAMHDAGTYDVTFRGGANGSIRYEE 63
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 6 PTVSEYKKAIDAKRKRLGLIAEKNCAPIMRLAMHSAGTYDVTFRGGANGSIRYEE 65
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 64 YTHGSNAGIKTAIDLEPIKAKHPRTYADLHQLAGVAAVEVTGGPTVEFTIGRRDSSVC 123
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 66 LAHGANNGLIDIVALLREPIKEQFPIISYADFQLAGVAAVEVTGGPTVEFTIGRRDSSVC 125
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 124 PREGRLPAKKGAPHLRDIYFR-MGLTPKDIYALSGHSLGKAHBERSGFDGAMTRDPLK 182
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 126 PEGRLPAGKSGDHLRVEFGKTMGLSDODIVALLSGHSLGKAHBERSGFDGAMTRDPLK 185
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 183 FDNSTFLELLGSESGLLKLPDALKLDDPEFRVVELYANDEVFFKDYAESHKLSSEL 242
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 186 FDNSTFVLLSGEKGLQLPDKALLDSDPVRPLVEKYADEDAFFADYALHQRSEL 245
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 243 GF 244
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 246 GF 247
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 11
866214
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D86214
R:Phellogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: D86214
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-250 <STO>
A:Cross-references: GB:AE05172; NID:98439880; PIDN:AA75066.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: cytochrome-c peroxidase

Query Match 54.6%; Score 818.5; DB 2; Length 250;
Best Local Similarity 63.6%; Pred. No. 2.3e-60;
Matches 154; Conservative 32; Mismatches 55; Indels 1; Gaps 1;

4 PVVDAEYLROVDARRARALIASKCAPIMRLAMHDAGTYDVTFRGGANGSIRYEE 63
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 6 PTVSEYKKAIDAKRKRLGLIAEKNCAPIMRLAMHSAGTYDVTFRGGANGSIRYEE 65
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 64 YTHGSNAGIKTAIDLEPIKAKHPRTYADLHQLAGVAAVEVTGGPTVEFTIGRRDSSVC 123
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 66 LAHGANNGLIDIVALLREPIKEQFPIISYADFQLAGVAAVEVTGGPTVEFTIGRRDSSVC 125
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 124 PREGRLPAKKGAPHLRDIYFR-MGLTPKDIYALSGHSLGKAHBERSGFDGAMTRDPLK 182
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 126 PEGRLPAGKSGDHLRVEFGKTMGLSDODIVALLSGHSLGKAHBERSGFDGAMTRDPLK 185
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 183 FDNSTFLELLGSESGLLKLPDALKLDDPEFRVVELYANDEVFFKDYAESHKLSSEL 242
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 186 FDNSTFVLLSGEKGLQLVSDKALLDSDPVRPLVEKYADEDAFFADYAEAHMKLSSEL 245
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 243 GF 244
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 246 GF 247
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 12
520866
L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)
N:Contains: L-ascorbate peroxidase cytosolic precursor
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Jun-1993 #sequence_revision 18-Jun-1993 #text_change 21-Jul-2000
R:Kubo, A.; Saji, H.; Tanaka, K.; Tanaka, K.; Kondo, N.
Plant Mol. Biol. 18, 691-701, 1992
A:Title: Cloning and sequencing of a cDNA encoding ascorbate peroxidase from Arabidop
A:Reference number: S20866; MUID:92216045
A:Accession: S20866
A:Molecule type: mRNA
A:Residues: 1-263 <KUB1>
A:Cross-references: EMBL:X59600; NID:916172
A:Accession: S32586
A:Molecule type: protein
A:Residues: 15-31 <KUB2>
R:Kubo, A.; Saji, H.; Tanaka, K.; Kondo, N.
FEBS Lett. 315, 313-317, 1993
A:Title: Genomic DNA structure of a gene encoding cytosolic ascorbate peroxidase from
A:Reference number: S28856; MUID:93138095
A:Accession: S28856
A:Molecule type: DNA
A:Residues: 14-263 <KUB3>
A:Cross-references: EMBL:D14442; NID:9217832; PIDN:BA00334.1; PID:9217833
C:Genetics:
A:Introns: 53/2; 111/3; 133/3; 178/3; 205/2; 239/3; 259/2
C:Superfamily: cytochrome-c peroxidase
C:Keywords: alternative initiators; chloroplast; chromoprotein; cytosol; heme; iron;
F:1-14/Domain: transit peptide (chloroplast) (fragment) #status predicted <TNP>
F:15-263/Product: L-ascorbate peroxidase cytosolic precursor #status predicted <PREC>
F:15-263/Product: L-ascorbate peroxidase #status experimental <MAT>
F:15/Active site: His (distal axial ligand) #status predicted
F:176/Binding site: heme iron (His) (proximal axial ligand) #status predicted
F:192,221/Active site: Trp, Asp #status predicted

Query Match 54.6%; Score 818.5; DB 2; Length 263;
Best Local Similarity 63.6%; Pred. No. 2.5e-60;
Matches 154; Conservative 32; Mismatches 55; Indels 1; Gaps 1;

4 PVVDAEYLROVDARRARALIASKCAPIMRLAMHDAGTYDVTFRGGANGSIRYEE 63
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 19 PTVSEYKKAIDAKRKRLGLIAEKNCAPIMRLAMHSAGTYDVTFRGGANGSIRYEE 78
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 64 YTHGSNAGIKTAIDLEPIKAKHPRTYADLHQLAGVAAVEVTGGPTVEFTIGRRDSSVC 123
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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Db 79 QAHGANSIHTALRLDPIRQGFPTISFADBNHLAGVAVETGGPDIRPHNREDKRP 138
QY 124 PREGRLPAKKGAHRLDIPR-MGLTDKDIVALSGSHSGKAHPERSGFDGAWTRDPLK 182
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 139 PPRELRPATGGCHLRLDVFKAQKSLDSDKDIVALSGAHTGCRCHKDRSGEGEAWTNSPLT 198
QY 183 FDNSTFLELLKGSEBGLKLPDTRDALLDDDEFRKYVLYLAKDEVDYFFKDAESHKLSL 242
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 199 FDNSTYFELLSGEKGLQLVSDKALLDDPVFRPLYERKVAADBDPAFADAEAHMKLSL 258
QY 243 GF 244
    | |
Db 259 GF 260

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RESULT 13
S43157
L-ascorbate peroxidase (EC 1.11.1.11) - radish
C:Species: *Raphanus sativus* (radish)
C:Date: 20-May-1994 #sequence-Revision 10-Nov-1995 #text-change 19-May-2000
C:Accession: S43157
R:Lopez, F.; Vansuyt, G.; Fourcroy, P.; Casse-Delbart, F.
submitted to the EMBL Data Library, March 1994
A:Description: Ascorbate peroxidase is induced in salt-stressed *Raphanus sativus*
A:Reference number: S43157
Accession: S43157

A:Cross-references: EMBL:X78457; NID:g466732; PID:g466733
C:Superfamily: cytochrome-c peroxidase
C:Keywords: chromoprotein; heme; Iron; metalloprotein; oxidoreductase
F:44/Active site: His (distal axial ligand) #status predicted
F:163/Binding site: heme iron (His) (proximal axial ligand) #status predicted
F:119,208/Active site: Trp, Asp #status predicted

Query Match	54.4%	Score 815.5	DB 2	Length 250	.
Best Local Similarity	63.2%	Pred. No. 4.1e-60			
Matches 153	Conservative 33	Mismatches 55		Indels 1	Gaps 1

[illegible]

RESULT 14
A45116
L-ascorbate peroxidase (EC 1.11.1.11), cytosolic [validated] - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C:Accession: A45116: S17553
R:Mittler, R.; Zilinskas, B.A.
J. Biol. Chem. 267, 21802-21807, 1992
A:Title: Molecular cloning and characterization of a gene encoding pea cytosolic ascorbate peroxidase
A:Reference number: A45116; MUID:93016138
A:Accession: A45116
A:Status: not compared with conceptual translation
A:Molecule type: DNA

A:Residues: 150 <MT>
A:Cross-references: GB:M03051; NID:g169042; PIDD:AAA33645.1; PID:g169043
A:Experimental source: cv Alaska
A:Note: sequence extracted from NCBI backbone (NCBIP:116752)
R:Mittler, R.; Zilinskas, B.A.
FEBS Lett. 289, 257-259, 1991
A:Title: Molecular cloning and nucleotide sequence analysis of a cDNA encoding pea cy
A:Reference number: S17553; MUID:92008636
A:Accession: S17553

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-152, 'VV', 154-250 <MI2>
A:Cross-references: EMBL:X62077; NID:920647
A:Note: the sequence is revised in GenBank entry PSAPXI, release 113.0, PID:X620648, P
R:Patterson, W.R., Poulos, T.L.
submitted to the Brookhaven Protein Data Bank, February 1995
A:Reference number: A6511; PDB:1APX
A:Contents: annotation, x-ray crystallography, 2.2 angstroms, residues 2-250
A:Note: recombinant form expressed in *Escherichia coli*

A:Reference number: A58672: MUID:95217899
A:Title: Crystal structure of recombinant pea cytosolic ascorbate peroxidase.
R:Paterson, W.R.; Poulos, T.L.
Biochemistry 34, 4331-4341, 1995

A:Contents: annotation; X-ray crystallography. 2.2 angstroms
A:Note: evidence is discussed that a free radical intermediate is formed by the heme
C:Genetics:
A:Gene: Apx1
A:Introns: 40/2; 98/3; 120/3; 137/1; 165/3; 192/2; 226/3; 246/2

A:Function: A:Description: catalyzes the oxidation by hydrogen peroxidase of two molecules of asc
C:Superfamily: cytochrome-c peroxidase
E:2_250/Product: L-ascorbate peroxidase cytosolic isozyme #status experimental <MAR>
F:4/Active site: His (distal axial ligand) #status predicted
F:13/Binding site: heme iron (His) (proximal axial ligand) #status experimental
F:19/Active site: Trp, Asp #status predicted

Query Match 53.6%; Score 802.5; DB 2; Length 250;
Best Local Similarity 62.8%; Pred. No. 4,96-59;
Matches 152; Conservative 34; Mismatches 55; Indels 1; Gaps 1.

QY	4	PVVDATYELQVDRARRAEFALIAKSGAPIMLRAMHMDGATDVNTRTGGANGSIRYEE	63
		: : : : : : : : : : : : : : : : : : : :	
Db	6	PTVSPYQAIKAIKARKRKIRGEIAEKKCAPILRLAMHMSGFEDSKTKGPGFTIKQAE	65
QY	64	YTVGSNAGLKIKIDLEPIIKAKHPKITYADLOHACVAVAEVTGKPTVEPIPSGRDSVC	123
		: : : : : : : : : : : : : : : : : : : : :	
Db	66	IAHGANGDIDIVALLIEPIKQFPVSYADPFOAGVAVETTGGEVPTFHGKEDPEP	125
QY	124	PREGRLPDAAKKGAPHLRIDIEFR-MGLTDKDIVALSGSHLGAHPERSGEFGDANTPLK	182
		: : : : : : : : : : : : : : : : : : : : : : : :	
Db	126	PPRGRIPLDPAITKSDHLRIYVFKAMGLSDODIVALSGHITGAHNERSGFPGPMTSNPLI	185
QY	183	FDRSYELTELLIKESGGLKLEPTDKALLDDEFFARYVELAKNEDVFFDFVSESKTKSEL	242
		: : : : : : : : : : : : : : : : : : : : : : : :	
Db	186	FDMSTYELTELLTEKNGLLQLESDKALLTDSVFRIYVEKTAADVDVFFADYEAHLKSEL	245
QY	243	GF 244	
		:	
Db	246	GF 247	
		:	

RESULT 15
T12389
L:Ascorbate peroxidase (EC 1.11.1.11) - common ice plant
C:Species: Mesembryanthemum crystallinum (common ice plant)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 17-Mar-2000
C:Accession: T12389
R:Michalowski, C.B.; Bohner, H.J.
Submitted to the EMBL Data Library, December 1995
A:Reference number: Z17504
A:Accession: T12389
A:Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-260 <MI

A;Residues: 1-260 <MIC>

A;Cross-references: EMBL:U43561; NID:g1171211; PID:g1171212

C;Genetics:

A; Gene: Apx

C;Function:

A;Description: catalyzes peroxidation of ascorbate to dehydroascorbate

C;Superfamily: cytochrome-c peroxidase

C;Keywords: heme; iron; metalloprotein; oxidoreductase

F;155/Blinding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match	Score	DB	Length
51.88	775.5	2	260

Best Local Similarity 57.08; Pred. No. 8.9e-57;

Matches 142; Conservative 44; Mismatches 62; Indels 1; Gaps 1;

[illegible]

Search completed: October 23, 2002, 13:58:05
Job time : 19 secs

